

## SEQUENCE LISTING

&lt;110&gt; Garvan Institute of Medical Research

&lt;120&gt; Methods for the diagnosis and prognosis of ovarian cancer

&lt;130&gt; 501731/MRO

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&lt;210&gt; 1

&lt;211&gt; 3432

&lt;212&gt; DNA

&lt;213&gt; NM\_005460 SNCAIP, synphilin

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&lt;221&gt; CDS

&lt;222&gt; (94)..(2850)

&lt;223&gt;

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 Gly Ile Ala Asp Val Tyr Ser Lys Phe Arg Pro Val Lys Arg Val Ser  
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 Pro Leu Lys His Gln Pro Glu Thr Leu Glu Asn Asn Glu Ser Asp Asp  
 85 90 95  
 Gln Lys Asn Gln Lys Val Val Glu Tyr Gln Lys Gly Gly Glu Ser Asp  
 100 105 110  
 Leu Gly Pro Gln Pro Gln Glu Leu Gly Pro Gly Asp Gly Val Gly Gly  
 115 120 125  
 Pro Pro Gly Lys Ser Ser Glu Pro Ser Thr Ser Leu Gly Glu Leu Glu  
 130 135 140  
 His Tyr Asp Leu Asp Met Asp Glu Ile Leu Asp Val Pro Tyr Ile Lys  
 145 150 155 160  
 Ser Ser Gln Gln Leu Ala Ser Phe Thr Lys Val Thr Ser Glu Lys Arg  
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 Ile Leu Gly Leu Cys Thr Thr Ile Asn Gly Leu Ser Gly Lys Ala Cys  
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Ser Thr Gly Ser Ser Glu Ser Ser Ser Ser Asn Met Ala Pro Phe Cys  
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Val Leu Ser Pro Val Lys Ser Pro His Leu Arg Lys Ala Ser Ala Val  
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Ile His Asp Gln His Lys Leu Ser Thr Glu Glu Thr Glu Ile Ser Pro  
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Lys Thr Thr Pro Asp Cys Gln Leu Arg Ala Phe His Leu Gln Ser Ser  
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Leu Thr Ser Leu Met Gly Glu Asp Cys Leu Asn Glu Arg Asn Thr Glu  
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Lys Leu Thr Pro Ala Gly Leu Ala Ile Lys Asn Gly Gln Leu Glu Cys  
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Val Arg Trp Met Val Ser Glu Thr Glu Ala Ile Ala Glu Leu Ser Cys  
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Glu Lys Ile Leu Leu Trp Leu Leu Gln Phe Met Gln Glu Gln Gly Ile  
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Ser Leu Asp Glu Val Asp Gln Asp Gly Asn Ser Ala Val His Val Ala  
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Pro Lys Ala Lys Asp Glu Asp Ser Asp Lys Ile Leu Arg Gln Leu Leu  
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Gly Lys Glu Ile Ser Glu Asn Val Cys Thr Gln Glu Lys Leu Ser Leu  
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785 790 795 800

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850 855 860

Arg Ser Ile Met Glu Thr Leu Ser Gly Asn Gln Asn Asn Asn Asn Asn  
865 870 875 880

Tyr Gln Ala Ala Asn Gln Leu Lys Thr Ser Thr Leu Pro Leu Thr Ser  
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Val Gln Glu Arg Thr Thr Leu Arg Tyr Glu Glu Arg Ile Thr Glu Leu  
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gcg gtc aag ctg acc atg ctg gag ctg gaa agc atc cac atc gat cct Ala Val Lys Leu Thr Met Leu Glu Leu Glu Ser Ile His Ile Asp Pro 585 590 595	2011
ctc agc tat gac gtc aag cct cgg gga gac agc cag agg ctg gat ctg Leu Ser Tyr Asp Val Lys Pro Arg Gly Asp Ser Gln Arg Leu Asp Leu 600 605 610	2059
gaa aac gca gtg ctt atg cag gag ctc atg gcc atg aag gag gag atg Glu Asn Ala Val Leu Met Gln Glu Leu Met Ala Met Lys Glu Glu Met 615 620 625	2107
gcc gag ttg aag gcc cag ctc tac cta ctg gag aaa gag aag aag gcc Ala Glu Leu Lys Ala Gln Leu Tyr Leu Leu Glu Lys Glu Lys Lys Ala 630 635 640 645	2155
ctg gag ctg aag ctg agc acg cgg gag gcc cag gag cag gcc tac ctg Leu Glu Leu Lys Leu Ser Thr Arg Glu Ala Gln Glu Gln Ala Tyr Leu 650 655 660	2203
gtg cac att gag cac ctg aag tcc gag gtg gag gag cag aag gag cag Val His Ile Glu His Leu Lys Ser Glu Val Glu Glu Gln Lys Glu Gln 665 670 675	2251
cgg atg cga tcc ctc agc tcc acc agc agc ggc agc aaa gat aaa cct Arg Met Arg Ser Leu Ser Ser Thr Ser Ser Gly Ser Lys Asp Lys Pro 680 685 690	2299
ggc aag gag tgt gct gat gct gcc tcc cca gct ctg tcc cta gct gaa Gly Lys Glu Cys Ala Asp Ala Ala Ser Pro Ala Leu Ser Leu Ala Glu 695 700 705	2347
ctc agg aca acg tgc agc gag aat gag ctg gct gcg gag ttc acc aac Leu Arg Thr Thr Cys Ser Glu Asn Glu Leu Ala Ala Glu Phe Thr Asn 710 715 720 725	2395
gcc att cgt cga gaa aag aag ttg aag gcc aga gtt caa gag ctg gtg Ala Ile Arg Arg Glu Lys Lys Leu Lys Ala Arg Val Gln Glu Leu Val 730 735 740	2443
agt gcc ttg gag aga ctc acc aag agc agt gaa atc cga cat cag caa Ser Ala Leu Glu Arg Leu Thr Lys Ser Ser Glu Ile Arg His Gln Gln 745 750 755	2491
tct gca gag ttc gtg aat gat cta aag cgg gcc aac agc aac ctg gtg Ser Ala Glu Phe Val Asn Asp Leu Lys Arg Ala Asn Ser Asn Leu Val 760 765 770	2539

gct gcc tat gag aaa gca aag aaa aag cat caa aac aaa ctg aag aag	2587
Ala Ala Tyr Glu Lys Ala Lys Lys Lys His Gln Asn Lys Leu Lys Lys	
775 780 785	
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Leu Glu Ser Gln Met Met Ala Met Val Glu Arg His Glu Thr Gln Val	
790 795 800 805	
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Arg Met Leu Lys Gln Arg Ile Ala Leu Leu Glu Glu Glu Asn Ser Arg	
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cca cac acc aat gaa act tcg ctt taatcagcac tcacgcaccg gagttctgcc	2737
Pro His Thr Asn Glu Thr Ser Leu	
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&lt;211&gt; 829

&lt;212&gt; PRT

&lt;213&gt; NM\_002387 MCC, mutated in colorectal cancers

&lt;400&gt; 4

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Val Glu Leu Asn Lys Arg Leu Gln Gln Thr Glu Arg Glu Arg Asp Leu  
 35 40 45

Leu Glu Lys Lys Leu Ala Lys Ala Gln Cys Glu Gln Ser His Leu Met  
 50 55 60

Arg Glu His Glu Asp Val Gln Glu Arg Thr Thr Leu Arg Tyr Glu Glu  
 65 70 75 80

Arg Ile Thr Glu Leu His Ser Val Ile Ala Glu Leu Asn Lys Lys Ile  
 85 90 95

Asp Arg Leu Gln Gly Thr Thr Ile Arg Glu Glu Asp Glu Tyr Ser Glu  
 100 105 110

Leu Arg Ser Glu Leu Ser Gln Ser Gln His Glu Val Asn Glu Asp Ser  
 115 120 125

Arg Ser Met Asp Gln Asp Gln Thr Ser Val Ser Ile Pro Glu Asn Gln  
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Ser Thr Met Val Thr Ala Asp Met Asp Asn Cys Ser Asp Leu Asn Ser  
 145 150 155 160

Glu Leu Gln Arg Val Leu Thr Gly Leu Glu Asn Val Val Cys Gly Arg  
 165 170 175

Lys Lys Ser Ser Cys Ser Leu Ser Val Ala Glu Val Asp Arg His Ile  
 180 185 190

Glu Gln Leu Thr Thr Ala Ser Glu His Cys Asp Leu Ala Ile Lys Thr  
 195 200 205

Val Glu Glu Ile Glu Gly Val Leu Gly Arg Asp Leu Tyr Pro Asn Leu  
 210 215 220

Ala Glu Glu Arg Ser Arg Trp Glu Lys Glu Leu Ala Gly Leu Arg Glu  
225 230 235 240

Glu Asn Glu Ser Leu Thr Ala Met Leu Cys Ser Lys Glu Glu Glu Leu  
245 250 255

Asn Arg Thr Lys Ala Thr Met Asn Ala Ile Arg Glu Glu Arg Asp Arg  
260 265 270

Leu Arg Arg Arg Val Arg Glu Leu Gln Thr Arg Leu Gln Ser Val Gln  
275 280 285

Ala Thr Gly Pro Ser Ser Pro Gly Arg Leu Thr Ser Thr Asn Arg Pro  
290 295 300

Ile Asn Pro Ser Thr Gly Glu Leu Ser Thr Ser Ser Ser Ser Asn Asp  
305 310 315 320

Ile Pro Ile Ala Lys Ile Ala Glu Arg Val Lys Leu Ser Lys Thr Arg  
325 330 335

Ser Glu Ser Ser Ser Ser Asp Arg Pro Val Leu Gly Ser Glu Ile Ser  
340 345 350

Ser Ile Gly Val Ser Ser Ser Val Ala Glu His Leu Ala His Ser Leu  
355 360 365

Gln Asp Cys Ser Asn Ile Gln Glu Ile Phe Gln Thr Leu Tyr Ser His  
370 375 380

Gly Ser Ala Ile Ser Glu Ser Lys Ile Arg Glu Phe Glu Val Glu Thr  
385 390 395 400

Glu Arg Leu Asn Ser Arg Ile Glu His Leu Lys Ser Gln Asn Asp Leu  
405 410 415

Leu Thr Ile Thr Leu Glu Glu Cys Lys Ser Asn Ala Glu Arg Met Ser  
420 425 430

Met Leu Val Gly Lys Tyr Glu Ser Asn Ala Thr Ala Leu Arg Leu Ala  
435 440 445

Leu Gln Tyr Ser Glu Gln Cys Ile Glu Ala Tyr Glu Leu Leu Ala  
450 455 460

Leu Ala Glu Ser Glu Gln Ser Leu Ile Leu Gly Gln Phe Arg Ala Ala  
465 470 475 480

Gly Val Gly Ser Ser Pro Gly Asp Gln Ser Gly Asp Glu Asn Ile Thr  
485 490 495

Gln Met Leu Lys Arg Ala His Asp Cys Arg Lys Thr Ala Glu Asn Ala  
500 505 510

Ala Lys Ala Leu Leu Met Lys Leu Asp Gly Ser Cys Gly Gly Ala Phe  
515 520 525

Ala Val Ala Gly Cys Ser Val Gln Pro Trp Glu Ser Leu Ser Ser Asn  
530 535 540

Ser His Thr Ser Thr Thr Ser Ser Thr Ala Ser Ser Cys Asp Thr Glu  
545 550 555 560

Phe Thr Lys Glu Asp Glu Gln Arg Leu Lys Asp Tyr Ile Gln Gln Leu  
565 570 575

Lys Asn Asp Arg Ala Ala Val Lys Leu Thr Met Leu Glu Leu Glu Ser  
580 585 590

Ile His Ile Asp Pro Leu Ser Tyr Asp Val Lys Pro Arg Gly Asp Ser  
595 600 605

Gln Arg Leu Asp Leu Glu Asn Ala Val Leu Met Gln Glu Leu Met Ala  
610 615 620

Met Lys Glu Glu Met Ala Glu Leu Lys Ala Gln Leu Tyr Leu Leu Glu  
625 630 635 640

Lys Glu Lys Lys Ala Leu Glu Leu Lys Leu Ser Thr Arg Glu Ala Gln  
645 650 655

Glu Gln Ala Tyr Leu Val His Ile Glu His Leu Lys Ser Glu Val Glu  
660 665 670

Glu Gln Lys Glu Gln Arg Met Arg Ser Leu Ser Ser Thr Ser Ser Gly  
675 680 685

Ser Lys Asp Lys Pro Gly Lys Glu Cys Ala Asp Ala Ala Ser Pro Ala  
690 695 700

Leu Ser Leu Ala Glu Leu Arg Thr Thr Cys Ser Glu Asn Glu Leu Ala  
705 710 715 720

Ala Glu Phe Thr Asn Ala Ile Arg Arg Glu Lys Lys Leu Lys Ala Arg  
725 730 735

Val Gln Glu Leu Val Ser Ala Leu Glu Arg Leu Thr Lys Ser Ser Glu  
740 745 750

Ile Arg His Gln Gln Ser Ala Glu Phe Val Asn Asp Leu Lys Arg Ala  
755 760 765

Asn Ser Asn Leu Val Ala Ala Tyr Glu Lys Ala Lys Lys Lys His Gln  
 770 775 780

Asn Lys Leu Lys Lys Leu Glu Ser Gln Met Met Ala Met Val Glu Arg  
 785 790 795 800

His Glu Thr Gln Val Arg Met Leu Lys Gln Arg Ile Ala Leu Leu Glu  
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Glu Glu Asn Ser Arg Pro His Thr Asn Glu Thr Ser Leu  
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 gcgggtcgcc atg gac cgc cca gat gag ggg cct ccg gcc aag acc cgc cgc 171  
 Met Asp Arg Pro Asp Glu Gly Pro Pro Ala Lys Thr Arg Arg  
 1 5 10  
 ctg agc agc tcc gag tct cca cag cgc gac ccg ccc ccg ccg ccg ccg 219  
 Leu Ser Ser Ser Glu Ser Pro Gln Arg Asp Pro Pro Pro Pro Pro Pro  
 15 20 25 30  
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 Pro Pro Pro Leu Leu Arg Leu Pro Leu Pro Pro Pro Gln Gln Arg Pro  
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 agg ctc cag gag gaa acg gag gcg gca cag gtg ctg gcc gat atg agg 315  
 Arg Leu Gln Glu Glu Thr Glu Ala Ala Gln Val Leu Ala Asp Met Arg  
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 ggg gtg gga ctg ggc ccc gcg ctg ccc ccg ccg cct ccc tat gtc att 363  
 Gly Val Gly Leu Gly Pro Ala Leu Pro Pro Pro Pro Pro Tyr Val Ile  
 65 70 75  
 ctc gag gag ggg ggg atc cgc gca tac ttc acg ctc ggt gct gag tgt 411  
 Leu Glu Glu Gly Gly Ile Arg Ala Tyr Phe Thr Leu Gly Ala Glu Cys  
 80 85 90  
 ccc gcc tgg gat tct acc atc gag tcg ggg tat ggg gag gcg ccc ccg 459  
 Pro Gly Trp Asp Ser Thr Ile Glu Ser Gly Tyr Gly Glu Ala Pro Pro



95		100		105		110	
ccc acg gag agc ctg gaa gca ctc ccc act cct gag gcc tcg ggg ggg							507
Pro Thr Glu Ser Leu Glu Ala Leu Pro Thr Pro Glu Ala Ser Gly Gly							
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agc ctg gaa atc gat ttt cag gtt gta cag tcg agc agt ttt ggt gga							555
Ser Leu Glu Ile Asp Phe Gln Val Val Gln Ser Ser Ser Phe Gly Gly							
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gag ggg gcc cta gaa acc tgt agc gca gtg ggg tgg gcg ccc cag agg							603
Glu Gly Ala Leu Glu Thr Cys Ser Ala Val Gly Trp Ala Pro Gln Arg							
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tta gtt gac ccg aag agc aag gaa gag gcg atc atc ata gtg gag gat							651
Leu Val Asp Pro Lys Ser Lys Glu Glu Ala Ile Ile Ile Val Glu Asp							
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cgg cgg cgg agg agg aag cag agg aag gtg aag agg gaa agc aga gag							747
Arg Arg Arg Arg Arg Lys Gln Arg Lys Val Lys Arg Glu Ser Arg Glu							
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aga aat gcc gag agg atg gag agc atc ctg cag gca ctg gag gat att							795
Arg Asn Ala Glu Arg Met Glu Ser Ile Leu Gln Ala Leu Glu Asp Ile							
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cag ctg gat ctg gag gca gtg aac atc aag gca ggc aaa gcc ttc ctg							843
Gln Leu Asp Leu Glu Ala Val Asn Ile Lys Ala Gly Lys Ala Phe Leu							
		225		230		235	
cgt ctc aag cgc aag ttc atc cag atg cga aga ccc ttc ctg gag cgc							891
Arg Leu Lys Arg Lys Phe Ile Gln Met Arg Arg Pro Phe Leu Glu Arg							
		240		245		250	
aga gac ctc atc atc cag cat atc cca ggc ttc tgg gtc aaa gca ttc							939
Arg Asp Leu Ile Ile Gln His Ile Pro Gly Phe Trp Val Lys Ala Phe							
		255		260		265	270
ctc aac cac ccc aga att tca att ttg atc aac cga cgt gat gaa gac							987
Leu Asn His Pro Arg Ile Ser Ile Leu Ile Asn Arg Arg Asp Glu Asp							
		275		280		285	
att ttc cgc tac ttg acc aat ctg cag gta cag gat ctc aga cat atc							1035
Ile Phe Arg Tyr Leu Thr Asn Leu Gln Val Gln Asp Leu Arg His Ile							
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tcc atg ggc tac aaa atg aag ctg tac ttc cag act aac ccc tac ttc							1083
Ser Met Gly Tyr Lys Met Lys Leu Tyr Phe Gln Thr Asn Pro Tyr Phe							
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aca aac atg gtg att gtc aag gag ttc cag cgc aac cgc tca ggc cgg							1131
Thr Asn Met Val Ile Val Lys Glu Phe Gln Arg Asn Arg Ser Gly Arg							
		320		325		330	
ctg gtg tct cac tca acc cca atc cgc tgg cac cgg ggc cag gaa ccc							1179
Leu Val Ser His Ser Thr Pro Ile Arg Trp His Arg Gly Gln Glu Pro							
		335		340		345	350
cag gcc cgt cgt cac ggg aac cag gat gcg agc cac agc ttt ttc agc							1227
Gln Ala Arg Arg His Gly Asn Gln Asp Ala Ser His Ser Phe Phe Ser							
		355		360		365	
tgg ttc tca aac cat agc ctc cca gag gct gac agg att gct gag att							1275
Trp Phe Ser Asn His Ser Leu Pro Glu Ala Asp Arg Ile Ala Glu Ile							

370	375	380	
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agg ggc tcc agg ata aag aga aag aag caa gaa atg aag aaa cgt aaa Arg Gly Ser Arg Ile Lys Arg Lys Lys Gln Glu Met Lys Lys Arg Lys 400 405 410			1371
acc agg ggc aga tgt gag gtg gtg atc atg gaa gac gcc cct gac tat Thr Arg Gly Arg Cys Glu Val Val Ile Met Glu Asp Ala Pro Asp Tyr 415 420 425 430			1419
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gag acc act gac aat gag ata act gac atc aat gag aac atc tgc gac Glu Thr Thr Asp Asn Glu Ile Thr Asp Ile Asn Glu Asn Ile Cys Asp 465 470 475			1563
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aac aac gag agt gct gat gac cac gaa acc act gac aac aat gag agt Asn Asn Glu Ser Ala Asp Asp His Glu Thr Thr Asp Asn Asn Glu Ser 495 500 505 510			1659
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gaa ggc atc cag caa gat gag gac atc tat gag gaa gga aac tat gag Glu Gly Ile Gln Gln Asp Glu Asp Ile Tyr Glu Glu Gly Asn Tyr Glu			2091

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gag gaa gga agt gaa gat gtc tgg gaa gaa ggg gaa gat tcg gac gac 2139  
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 655 660 665 670

tct gac cta gag gat gtg ctt cag gtc cca aac ggt tgg gcc aat ccg 2187  
 Ser Asp Leu Glu Asp Val Leu Gln Val Pro Asn Gly Trp Ala Asn Pro  
 675 680 685

ggg aag agg ggg aaa acc gga taagggtttt ccccttttgg ggatcacctc 2238  
 Gly Lys Arg Gly Lys Thr Gly  
 690

tctgtatccc ccacccacta tcccatttgc cctctctctc agctagggcc acgcggtccc 2298

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&lt;212&gt; PRT

&lt;213&gt; NM\_022117 SE20-4

&lt;400&gt; 6

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Pro Leu Leu Arg Leu Pro Leu Pro Pro Pro Gln Gln Arg Pro Arg Leu  
 35 40 45

Gln Glu Glu Thr Glu Ala Ala Gln Val Leu Ala Asp Met Arg Gly Val  
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Gly Leu Gly Pro Ala Leu Pro Pro Pro Pro Pro Tyr Val Ile Leu Glu  
 65 70 75 80

Glu Gly Gly Ile Arg Ala Tyr Phe Thr Leu Gly Ala Glu Cys Pro Gly

85 90 95  
 Trp Asp Ser Thr Ile Glu Ser Gly Tyr Gly Glu Ala Pro Pro Pro Thr  
 100 105 110  
 Glu Ser Leu Glu Ala Leu Pro Thr Pro Glu Ala Ser Gly Gly Ser Leu  
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 Glu Ile Asp Phe Gln Val Val Gln Ser Ser Ser Phe Gly Gly Glu Gly  
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 Ala Leu Glu Thr Cys Ser Ala Val Gly Trp Ala Pro Gln Arg Leu Val  
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 Asp Pro Lys Ser Lys Glu Glu Ala Ile Ile Ile Val Glu Asp Glu Asp  
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 Glu Asp Glu Arg Glu Ser Met Arg Ser Ser Arg Arg Arg Arg Arg Arg  
 180 185 190  
 Arg Arg Arg Lys Gln Arg Lys Val Lys Arg Glu Ser Arg Glu Arg Asn  
 195 200 205  
 Ala Glu Arg Met Glu Ser Ile Leu Gln Ala Leu Glu Asp Ile Gln Leu  
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 Asp Leu Glu Ala Val Asn Ile Lys Ala Gly Lys Ala Phe Leu Arg Leu  
 225 230 235 240  
 Lys Arg Lys Phe Ile Gln Met Arg Arg Pro Phe Leu Glu Arg Arg Asp  
 245 250 255  
 Leu Ile Ile Gln His Ile Pro Gly Phe Trp Val Lys Ala Phe Leu Asn  
 260 265 270  
 His Pro Arg Ile Ser Ile Leu Ile Asn Arg Arg Asp Glu Asp Ile Phe  
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 Arg Tyr Leu Thr Asn Leu Gln Val Gln Asp Leu Arg His Ile Ser Met  
 290 295 300  
 Gly Tyr Lys Met Lys Leu Tyr Phe Gln Thr Asn Pro Tyr Phe Thr Asn  
 305 310 315 320  
 Met Val Ile Val Lys Glu Phe Gln Arg Asn Arg Ser Gly Arg Leu Val  
 325 330 335  
 Ser His Ser Thr Pro Ile Arg Trp His Arg Gly Gln Glu Pro Gln Ala  
 340 345 350  
 Arg Arg His Gly Asn Gln Asp Ala Ser His Ser Phe Phe Ser Trp Phe

355                      360                      365  
 Ser Asn His Ser Leu Pro Glu Ala Asp Arg Ile Ala Glu Ile Ile Lys  
 370                      375                      380  
 Asn Asp Leu Trp Val Asn Pro Leu Arg Tyr Tyr Leu Arg Glu Arg Gly  
 385                      390                      395                      400  
 Ser Arg Ile Lys Arg Lys Lys Gln Glu Met Lys Lys Arg Lys Thr Arg  
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 Val Glu Asp Ile Phe Ser Glu Ile Ser Asp Ile Asp Glu Thr Ile His  
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 Asp Ile Lys Ile Ser Asp Phe Met Glu Thr Thr Asp Tyr Phe Glu Thr  
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 Thr Asp Asn Glu Ile Thr Asp Ile Asn Glu Asn Ile Cys Asp Ser Glu  
 465                      470                      475                      480  
 Asn Pro Asp His Asn Glu Val Pro Asn Asn Glu Thr Thr Asp Asn Asn  
 485                      490                      495  
 Glu Ser Ala Asp Asp His Glu Thr Thr Asp Asn Asn Glu Ser Ala Asp  
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 Lys Gly Gly Phe Trp Gly Ser His Gly Asn Asn Gln Asp Ser Ser Asp  
 545                      550                      555                      560  
 Ser Asp Asn Glu Ala Asp Glu Ala Ser Asp Asp Glu Asp Asn Asp Gly  
 565                      570                      575  
 Asn Glu Gly Asp Asn Glu Gly Ser Asp Asp Asp Gly Asn Glu Gly Asp  
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 Asn Glu Gly Ser Asp Asp Asp Asp Arg Asp Ile Glu Tyr Tyr Glu Lys  
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 Val Ile Glu Asp Phe Asp Lys Asp Gln Ala Asp Tyr Glu Asp Val Ile  
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625                      630                      635                      640

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                                 645                                  650                                  655

Gly Ser Glu Asp Val Trp Glu Glu Gly Glu Asp Ser Asp Asp Ser Asp  
                                 660                                  665                                  670

Leu Glu Asp Val Leu Gln Val Pro Asn Gly Trp Ala Asn Pro Gly Lys  
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Arg Gly Lys Thr Gly  
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&lt;223&gt;

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									Met	Met	Gly	Gly	5	Ser	Ala	Asp	
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Lys	Ala	Thr	Ala	Ala	Ala	Ala	Ala	Ala	Ser	Leu	Leu	Ala	Asn	Gly	His		
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gac	ctg	gcg	gcg	gcc	atg	gcg	gtg	gac	aaa	agc	aac	cct	acc	tca	aag		1050
Asp	Leu	Ala	Ala	Ala	Met	Ala	Val	Asp	Lys	Ser	Asn	Pro	Thr	Ser	Lys		
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cac	aaa	agt	ggt	gct	gtg	gcc	agc	ctg	ctg	agc	aag	gca	gag	cgg	gcc		1098
His	Lys	Ser	Gly	Ala	Val	Ala	Ser	Leu	Leu	Ser	Lys	Ala	Glu	Arg	Ala		
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Thr	Glu	Leu	Ala	Ala	Glu	Gly	Gln	Leu	Thr	Leu	Gln	Gln	Phe	Ala	Gln		
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Ser	Thr	Glu	Met	Leu	Lys	Arg	Val	Val	Gln	Glu	His	Leu	Pro	Leu	Met		
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Ser	Glu	Ala	Gly	Ala	Gly	Leu	Pro	Asp	Met	Glu	Ala	Val	Ala	Gly	Ala		
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gaa	gcc	ctc	aat	ggc	cag	tcc	gac	ttc	ccc	tac	ctg	ggc	gct	ttc	ccc		1290
Glu	Ala	Leu	Asn	Gly	Gln	Ser	Asp	Phe	Pro	Tyr	Leu	Gly	Ala	Phe	Pro		
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Ile	Asn	Pro	Gly	Leu	Phe	Ile	Met	Thr	Pro	Ala	Gly	Val	Phe	Leu	Ala		
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Glu	Ser	Ala	Leu	His	Met	Ala	Gly	Leu	Ala	Glu	Tyr	Pro	Met	Gln	Gly		
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Glu	Leu	Ala	Ser	Ala	Ile	Ser	Ser	Gly	Lys	Lys	Lys	Arg	Lys	Arg	Cys		
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ggc	atg	tgc	gcg	ccc	tgc	cgg	cgg	cgc	atc	aac	tgc	gag	cag	tgc	agc		1482
Gly	Met	Cys	Ala	Pro	Cys	Arg	Arg	Arg	Ile	Asn	Cys	Glu	Gln	Cys	Ser		
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agt	tgt	agg	aat	cga	aag	act	ggc</										

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&lt;211&gt; 227

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&lt;213&gt; NM\_016463 HSPC195

&lt;400&gt; 8

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Asp Lys Ser Asn Pro Thr Ser Lys His Lys Ser Gly Ala Val Ala Ser
35           40           45

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Leu Leu Ser Lys Ala Glu Arg Ala Thr Glu Leu Ala Ala Glu Gly Gln
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Leu Thr Leu Gln Gln Phe Ala Gln Ser Thr Glu Met Leu Lys Arg Val
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Val Gln Glu His Leu Pro Leu Met Ser Glu Ala Gly Ala Gly Leu Pro
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Asp Met Glu Ala Val Ala Gly Ala Glu Ala Leu Asn Gly Gln Ser Asp
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Phe Pro Tyr Leu Gly Ala Phe Pro Ile Asn Pro Gly Leu Phe Ile Met  
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Thr Pro Ala Gly Val Phe Leu Ala Glu Ser Ala Leu His Met Ala Gly  
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Leu Ala Glu Tyr Pro Met Gln Gly Glu Leu Ala Ser Ala Ile Ser Ser  
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Gly Lys Lys Lys Arg Lys Arg Cys Gly Met Cys Ala Pro Cys Arg Arg  
165 170 175

Arg Ile Asn Cys Glu Gln Cys Ser Ser Cys Arg Asn Arg Lys Thr Gly  
180 185 190

His Gln Ile Cys Lys Phe Arg Lys Cys Glu Glu Leu Lys Lys Lys Pro  
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Met Thr Glu Tyr Leu Asn Phe Glu Lys Ser Ser Ser Val Ser Arg Tyr  
1 5 10 15

gga gcc tct caa gtt gaa gat atg ggg aat ata att tta gca atg att 153  
Gly Ala Ser Gln Val Glu Asp Met Gly Asn Ile Ile Leu Ala Met Ile  
20 25 30

tca gag cct tat aat cac agg ttt tca gat cca gag aga gtg aat tac 201  
Ser Glu Pro Tyr Asn His Arg Phe Ser Asp Pro Glu Arg Val Asn Tyr  
35 40 45

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cac atg ggg acc cgg tat att gag gtt tac aaa gca aca ggt gaa gat His Met Gly Thr Arg Tyr Ile Glu Val Tyr Lys Ala Thr Gly Glu Asp 130 135 140	489
ttc ctt aaa att gct ggt ggt act tcc aat gag gta gcc cag ttt ctc Phe Leu Lys Ile Ala Gly Gly Thr Ser Asn Glu Val Ala Gln Phe Leu 145 150 155 160	537
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&lt;211&gt; 358

&lt;212&gt; PRT

&lt;213&gt; NM\_017697 FLJ20171

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 Lys Phe Glu Ser Gly Thr Cys Ser Lys Met Glu Leu Ile Asp Asp Asn  
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 Thr Val Val Arg Ala Arg Gly Leu Pro Trp Gln Ser Ser Asp Gln Asp  
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 Ile Ala Arg Phe Phe Lys Gly Leu Asn Ile Ala Lys Gly Gly Ala Ala  
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 Phe Val Ser Glu Glu His Arg Asp Leu Ala Leu Gln Arg His Lys His  
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 His Met Gly Thr Arg Tyr Ile Glu Val Tyr Lys Ala Thr Gly Glu Asp  
 130 135 140  
 Phe Leu Lys Ile Ala Gly Gly Thr Ser Asn Glu Val Ala Gln Phe Leu  
 145 150 155 160  
 Ser Lys Glu Asn Gln Val Ile Val Arg Met Arg Gly Leu Pro Phe Thr  
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 Ala Thr Ala Glu Glu Val Val Ala Phe Phe Gly Gln His Cys Pro Ile  
 180 185 190  
 Thr Gly Gly Lys Glu Gly Ile Leu Phe Val Thr Tyr Pro Asp Gly Arg  
 195 200 205  
 Pro Thr Gly Asp Ala Phe Val Leu Phe Ala Cys Glu Glu Tyr Ala Gln  
 210 215 220  
 Asn Ala Leu Arg Lys His Lys Asp Leu Leu Gly Lys Arg Tyr Ile Glu  
 225 230 235 240  
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 245 250 255  
 Ser Ser Ala Pro Leu Ile Pro Leu Pro Thr Pro Pro Ile Ile Pro Val  
 260 265 270  
 Leu Pro Gln Gln Phe Val Pro Pro Thr Asn Val Arg Asp Cys Ile Arg  
 275 280 285  
 Leu Arg Gly Leu Pro Tyr Ala Ala Thr Ile Glu Asp Ile Leu Asp Phe  
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Leu Gly Glu Phe Ala Thr Asp Ile Arg Thr His Gly Val His Met Val  
 305 310 315 320

Leu Asn His Gln Gly Arg Pro Ser Gly Asp Ala Phe Ile Gln Met Lys  
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 1 5 10  
 ccg aac ccc gcc gtg tcc ttc ccg ccg ccc cgg gtc acc ctg ccc gcc 160  
 Pro Asn Pro Ala Val Ser Phe Pro Pro Pro Arg Val Thr Leu Pro Ala  
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 Gly Pro Asp Ile Leu Arg Thr Tyr Ser Gly Ala Phe Val Cys Leu Glu  
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 Thr Ser Leu His Asp Leu His Cys Asn Thr Thr Ile Thr Gly Gln Pro  
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 Arg Arg Trp Arg Pro  
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Gln Gly Trp Val Met Phe Val Ser Val Thr Ala Phe Phe Phe Ser Leu  
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Leu Phe Leu Gly Met Phe Leu Ser Gly Met Val Ala Gln Ile Asp Ala  
85 90 95

Asn Trp Asn Phe Leu Asp Phe Ala Tyr His Phe Thr Val Phe Val Phe  
100 105 110

Tyr Phe Gly Ala Phe Leu Leu Glu Ala Ala Ala Thr Ser Leu His Asp

115 120 125

Leu His Cys Asn Thr Thr Ile Thr Gly Gln Pro Leu Leu Ser Asp Asn  
130 135 140

Gln Tyr Asn Ile Asn Val Ala Ala Ser Ile Phe Ala Phe Met Thr Thr  
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Met Pro Arg Pro Glu Leu Pro Leu Pro Glu Gly Trp Glu Glu  
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gcg cgc gac ttc gac ggc aag gtc tac tac ata gac cac acg aac cgc 156  
Ala Arg Asp Phe Asp Gly Lys Val Tyr Tyr Ile Asp His Thr Asn Arg  
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Thr Thr Ser Trp Ile Asp Pro Arg Asp Arg Tyr Thr Lys Pro Leu Thr  
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Phe Ala Asp Cys Ile Ser Asp Glu Leu Pro Leu Gly Trp Glu Glu Ala  
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Tyr Asp Pro Gln Val Gly Asp Tyr Phe Ile Asp His Asn Thr Lys Thr  
65 70 75

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Thr Gln Ile Glu Asp Pro Arg Val Gln Trp Arg Arg Glu Gln Glu His  
80 85 90

atg ctg aag gat tac ctg gtg gtg gcc cag gag gct ctg agt gca caa 396  
Met Leu Lys Asp Tyr Leu Val Val Ala Gln Glu Ala Leu Ser Ala Gln  
95 100 105 110

aag gag atc tac cag gtg aag cag cag cgc ctg gag ctt gca cag cag 444



Lys	Glu	Ile	Tyr	Gln	Val	Lys	Gln	Gln	Arg	Leu	Glu	Leu	Ala	Gln	Gln		
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Glu	Tyr	Gln	Gln	Leu	His	Ala	Val	Trp	Glu	His	Lys	Leu	Gly	Ser	Gln		
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Val	Ser	Leu	Val	Ser	Gly	Ser	Ser	Ser	Ser	Ser	Lys	Tyr	Asp	Pro	Glu		
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atc	ctg	aaa	gct	gaa	att	gcc	act	gca	aaa	tcc	cgg	gtc	aac	aag	ctg		588
Ile	Leu	Lys	Ala	Glu	Ile	Ala	Thr	Ala	Lys	Ser	Arg	Val	Asn	Lys	Leu		
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aag	aga	gag	atg	gtt	cac	ctc	cag	cac	gag	ctg	cag	ttc	aaa	gag	cgt		636
Lys	Arg	Glu	Met	Val	His	Leu	Gln	His	Glu	Leu	Gln	Phe	Lys	Glu	Arg		
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Gly	Phe	Gln	Thr	Leu	Lys	Lys	Ile	Asp	Lys	Lys	Met	Ser	Asp	Ala	Gln		
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Gly	Ser	Tyr	Lys	Leu	Asp	Glu	Ala	Gln	Ala	Val	Leu	Arg	Glu	Thr	Lys		
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gcc	atc	aaa	aag	gct	att	acc	tgt	ggg	gaa	aag	gaa	aag	caa	gat	ctc		780
Ala	Ile	Lys	Lys	Ala	Ile	Thr	Cys	Gly	Glu	Lys	Glu	Lys	Gln	Asp	Leu		
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att	aag	agc	ctt	gcc	atg	ttg	aag	gac	ggc	ttc	cgc	act	gac	agg	ggg		828
Ile	Lys	Ser	Leu	Ala	Met	Leu	Lys	Asp	Gly	Phe	Arg	Thr	Asp	Arg	Gly		
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Ser	His	Ser	Asp	Leu	Trp	Ser	Ser	Ser	Ser	Ser	Leu	Glu	Ser	Ser	Ser		
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Phe	Pro	Leu	Pro	Lys	Gln	Tyr	Leu	Asp	Val	Ser	Ser	Gln	Thr	Asp	Ile		
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Arg	Leu	Arg	Leu	Arg	Tyr	Glu	Glu	Ala	Lys	Arg	Arg	Ile	Ala	Asn	Leu		
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aag	atc	cag	ctg	gcc	aag	ctt	gac	agt	gag	gcc	tgg	cct	ggg	gtg	ctg		1068
Lys	Ile	Gln	Leu	Ala	Lys	Leu	Asp	Ser	Glu	Ala	Trp	Pro	Gly	Val	Leu		
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gac	tca	gag	agg	gac	cgg	ctg	atc	ctt	atc	aac	gag	aag	gag	gag	ctg		1116
Asp	Ser	Glu	Arg	Asp	Arg	Leu	Ile	Leu	Ile	Asn	Glu	Lys	Glu	Glu	Leu		
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ctg	aag	gag	atg	cgc	ttc	atc	agc	ccc	cgc	aag	tgg	acc	cag	ggg	gag		1164
Leu	Lys	Glu	Met	Arg	Phe	Ile	Ser	Pro	Arg	Lys	Trp	Thr	Gln	Gly	Glu		
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Val	Glu	Gln	Leu	Glu	Met	Ala	Arg	Lys	Arg	Leu	Glu	Lys	Asp	Leu	Gln		
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ccc tcc cca ccc tgt tcc cct ctc atg gct gac ccc ctc ctg gct ggt Pro Ser Pro Pro Cys Ser Pro Leu Met Ala Asp Pro Leu Leu Ala Gly 545 550 555	1740
gat gcc ttc ctc aac tcc ttg gag ttt gaa gac ccg gag ctg agt gcc Asp Ala Phe Leu Asn Ser Leu Glu Phe Glu Asp Pro Glu Leu Ser Ala 560 565 570	1788
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Lys	Asn	Lys	Gln	Phe	Ala	Ile	Leu	Ile	Ile	Gln	Leu	Ser	Asn	Leu	Ser		
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Leu	Pro	Cys	Ser	Glu	Ser	Thr	Thr	Cys	Leu	Phe	Arg	Thr	Arg	Pro	Leu		
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Leu	Ala	Glu	Val	Cys	Arg	Ser	Gly	Glu	Arg	Ser	Thr	Arg	Trp	Tyr	Asn		
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Gln Gln Leu His Ala Val Trp Glu His Lys Leu Gly Ser Gln Val Ser  
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Lys Lys Ala Ile Thr Cys Gly Glu Lys Glu Lys Gln Asp Leu Ile Lys  
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Glu Arg Asp Arg Leu Ile Leu Ile Asn Glu Lys Glu Glu Leu Leu Lys  
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Lys Arg Asn Gln Leu Val Arg Glu Leu Glu Glu Ala Thr Arg Gln Val  
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Ala Thr Leu His Ser Gln Leu Lys Ser Leu Ser Ser Ser Met Gln Ser  
420 425 430

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Phe Leu Asn Ser Leu Glu Phe Glu Asp Pro Glu Leu Ser Ala Thr Leu  
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Cys Glu Leu Ser Leu Gly Asn Ser Ala Gln Glu Arg Tyr Arg Leu Glu  
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Glu Pro Gly Thr Glu Gly Lys Gln Leu Gly Gln Ala Val Asn Thr Ala  
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Gln Gly Cys Gly Leu Lys Val Ala Cys Val Ser Ala Ala Val Ser Asp  
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Glu Ser Val Ala Gly Asp Ser Gly Val Tyr Glu Ala Ser Val Gln Arg  
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Leu Gly Ala Ser Glu Ala Ala Ala Phe Asp Ser Asp Glu Ser Glu Ala  
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Val Gly Ala Thr Arg Ile Gln Ile Ala Leu Lys Tyr Asp Glu Lys Asn  
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Lys Gln Phe Ala Ile Leu Ile Ile Gln Leu Ser Asn Leu Ser Ala Leu  
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Leu Gln Gln Gln Asp Gln Lys Val Asn Ile Arg Val Ala Val Leu Pro  
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Ser Asp Thr Leu Val Phe Asn Glu Val Phe Trp Val Ser Met Ser Tyr  
725 730 735

Pro Ala Leu His Gln Lys Thr Leu Arg Val Asp Val Cys Thr Thr Asp  
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Arg Ser His Leu Glu Glu Cys Leu Gly Gly Ala Gln Ile Ser Leu Ala  
755 760 765

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770 775 780

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785 790 795 800

Val Met Ala Pro Ala Ser Gly Pro Ala Ser Thr Asp Ala Val Ser Ala  
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Leu Leu Glu Gln Thr Ala Val Glu Leu Glu Lys Arg Gln Glu Gly Arg  
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Glu Asn Glu Ala Val Ala Glu Glu Glu Glu Glu Val Glu Glu Glu  
850 855 860

Glu Gly Glu Glu Asp Val Phe Thr Glu Lys Ala Ser Pro Asp Met Asp  
865 870 875 880

Gly Tyr Pro Ala Leu Lys Val Asp Lys Glu Thr Asn Thr Glu Thr Pro  
885 890 895

Ala Pro Ser Pro Thr Val Val Arg Pro Lys Asp Arg Arg Val Gly Thr  
900 905 910

Pro Ser Gln Gly Pro Phe Leu Arg Gly Ser Thr Ile Ile Arg Ser Lys  
915 920 925

Thr Phe Ser Pro Gly Pro Gln Ser Gln Tyr Val Cys Arg Leu Asn Arg  
930 935 940

Ser Asp Ser Asp Ser Ser Thr Leu Ser Lys Lys Pro Pro Phe Val Arg  
945 950 955 960

Asn Ser Leu Glu Arg Arg Ser Val Arg Met Lys Arg Pro Ser Ser Val  
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Lys Ser Leu Arg Ser Glu Arg Leu Ile Arg Thr Ser Leu Asp Leu Glu  
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Leu Asp Leu Gln Ala Thr Arg Thr Trp His Ser Gln Leu Thr Gln Glu  
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Ile Ser Val Leu Lys Glu Leu Lys Glu Gln Leu Glu Gln Ala Lys  
 1010 1015 1020

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Asp Phe Tyr Asn Pro Val Val Pro Glu Ala Gln Lys Arg Glu Met Gly  
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Glu Leu Ser Lys Met Leu Gly Lys Ser Trp Lys Ala Leu Thr Leu Ala  
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Lys Pro Thr Pro Asp Leu Arg Ile Ser Ile Glu Asn Ser Glu Glu Ala 50 55 60		
Leu Thr Val His Ala Pro Phe Pro Ala Ala His Pro Ala Ser Arg Ser 65 70 75 80		
Phe Pro Asp Pro Arg Gly Leu Tyr His Phe Cys Leu Tyr Trp Asn Arg 85 90 95		
His Ala Gly Arg Leu His Leu Leu Tyr Gly Lys Arg Asp Phe Leu Leu 100 105 110		
Ser Asp Lys Ala Ser Ser Leu Leu Cys Phe Gln His Gln Glu Glu Ser 115 120 125		
Leu Ala Gln Gly Pro Pro Leu Leu Ala Thr Ser Val Thr Ser Trp Trp 130 135 140		
Ser Pro Gln Asn Ile Ser Leu Pro Ser Ala Ala Ser Phe Thr Phe Ser 145 150 155 160		
Phe His Ser Pro Pro His Thr Ala Ala His Asn Ala Ser Val Asp Met 165 170 175		
Cys Glu Leu Lys Arg Asp Leu Gln Leu Leu Ser Gln Phe Leu Lys His 180 185 190		
Pro Gln Lys Ala Ser Arg Arg Pro Ser Ala Ala Pro Ala Ser Gln Gln 195 200 205		
Leu Gln Ser Leu Glu Ser Lys Leu Thr Ser Val Arg Phe Met Gly Asp 210 215 220		
Met Val Ser Phe Glu Glu Asp Arg Ile Asn Ala Thr Val Trp Lys Leu 225 230 235 240		
Gln Pro Thr Ala Gly Leu Gln Asp Leu His Ile His Ser Arg Gln Glu 245 250 255		
Glu Glu Gln Ser Glu Ile Met Glu Tyr Ser Val Leu Leu Pro Arg Thr 260 265 270		
Leu Phe Gln Arg Thr Lys Gly Arg Ser Gly Glu Ala Glu Lys Arg Leu 275 280 285		
Leu Leu Val Asp Phe Ser Ser Gln Ala Leu Phe Gln Asp Lys Asn Ser		

290

295

300

Ser His Val Leu Gly Glu Lys Val Leu Gly Ile Val Val Gln Asn Thr  
 305 310 315 320

Lys Val Ala Asn Leu Thr Glu Pro Val Val Leu Thr Phe Gln His Gln  
 325 330 335

Leu Gln Pro Lys Asn Val Thr Leu Gln Cys Val Phe Trp Val Glu Asp  
 340 345 350

Pro Thr Leu Ser Ser Pro Gly His Trp Ser Ser Ala Gly Cys Glu Thr  
 355 360 365

Val Arg Arg Glu Thr Gln Thr Ser Cys Phe Cys Asn His Leu Thr Tyr  
 370 375 380

Phe Ala Val Leu Met Val Ser Ser Val Glu Val Asp Ala Val His Lys  
 385 390 395 400

His Tyr Leu Ser Leu Leu Ser Tyr Val Gly Cys Val Val Ser Ala Leu  
 405 410 415

Ala Cys Leu Val Thr Ile Ala Ala Tyr Leu Cys Ser Arg Val Pro Leu  
 420 425 430

Pro Cys Arg Arg Lys Pro Arg Asp Tyr Thr Ile Lys Val His Met Asn  
 435 440 445

Leu Leu Leu Ala Val Phe Leu Leu Asp Thr Ser Phe Leu Leu Ser Glu  
 450 455 460

Pro Val Ala Leu Thr Gly Ser Glu Ala Gly Cys Arg Ala Ser Ala Ile  
 465 470 475 480

Phe Leu His Phe Ser Leu Leu Thr Cys Leu Ser Trp Met Gly Leu Glu  
 485 490 495

Gly Tyr Asn Leu Tyr Arg Leu Val Val Glu Val Phe Gly Thr Tyr Val  
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Pro Gly Tyr Leu Leu Lys Leu Ser Ala Met Gly Trp Gly Phe Pro Ile  
 515 520 525

Phe Leu Val Thr Leu Val Ala Leu Val Asp Val Asp Asn Tyr Gly Pro  
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Ile Ile Leu Ala Val His Arg Thr Pro Glu Gly Val Ile Tyr Pro Ser  
 545 550 555 560

Met Cys Trp Ile Arg Asp Ser Leu Val Ser Tyr Ile Thr Asn Leu Gly  
565 570 575

Leu Phe Ser Leu Val Phe Leu Phe Asn Met Ala Met Leu Ala Thr Met  
580 585 590

Val Val Gln Ile Leu Arg Leu Arg Pro His Thr Gln Lys Trp Ser His  
595 600 605

Val Leu Thr Leu Leu Gly Leu Ser Leu Val Leu Gly Leu Pro Trp Ala  
610 615 620

Leu Ile Phe Phe Ser Phe Ala Ser Gly Thr Phe Gln Leu Val Val Leu  
625 630 635 640

Tyr Leu Phe Ser Ile Ile Thr Ser Phe Gln Gly Phe Leu Ile Phe Ile  
645 650 655

Trp Tyr Trp Ser Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu  
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Lys Ser Asn Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr  
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Ser Ser Ser Arg Ile  
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<213> NM\_001307 claudin 7, CLDN7

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<222> (427)..(1059)

<223>

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tgtctggaac caccctcccg gcgtatccta ctccctgtgc cgcgaggcca tcgcttcact 240  
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ccaagtgtcg tttgttttac tgtaggtct cccgcccgcc gcccccagtg ttttctgagg 420

gcggaa atg gcc aat tgc gcc ctg cag ttg ctg gcc ttc tcc atg gcc 468  
Met Ala Asn Ser Gly Leu Gln Leu Leu Gly Phe Ser Met Ala  
1 5 10

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Leu Leu Gly Trp Val Gly Leu Val Ala Cys Thr Ala Ile Pro Gln Trp  
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cag atg agc tcc tat gcg ggt gac aac atc atc acg gcc cag gcc atg 564  
Gln Met Ser Ser Tyr Ala Gly Asp Asn Ile Ile Thr Ala Gln Ala Met  
35 40 45

tac aag ggg ctg tgg atg gac tgc gtc acg cag agc acg ggg atg atg 612  
Tyr Lys Gly Leu Trp Met Asp Cys Val Thr Gln Ser Thr Gly Met Met  
50 55 60

agc tgc aaa atg tac gac tgc gtg ctc gcc ctg tcc gcg gcc ttg cag 660  
Ser Cys Lys Met Tyr Asp Ser Val Leu Ala Leu Ser Ala Ala Leu Gln  
65 70 75

gcc act cga gcc cta atg gtg gtc tcc ctg gtg ctg gcc ttc ctg gcc 708  
Ala Thr Arg Ala Leu Met Val Val Ser Leu Val Leu Gly Phe Leu Ala  
80 85 90

atg ttt gtg gcc acg atg gcc atg aag tgc acg cgc tgt ggg gga gac 756  
Met Phe Val Ala Thr Met Gly Met Lys Cys Thr Arg Cys Gly Gly Asp  
95 100 105 110

gac aaa gtg aag aag gcc cgt ata gcc atg ggt gga gcc ata att ttc 804  
Asp Lys Val Lys Lys Ala Arg Ile Ala Met Gly Gly Gly Ile Ile Phe  
115 120 125

atc gtg gca ggt ctt gcc acc ttg gta gct tgc tcc tgg tat gcc cat 852  
Ile Val Ala Gly Leu Ala Thr Leu Val Ala Cys Ser Trp Tyr Gly His  
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cag att gtc aca gac ttt tat aac cct ttg atc cct acc aac att aag 900  
Gln Ile Val Thr Asp Phe Tyr Asn Pro Leu Ile Pro Thr Asn Ile Lys  
145 150 155

tat gag ttt gcc cct gcc atc ttt att gcc tgg gca ggg tct gcc cta 948  
Tyr Glu Phe Gly Pro Ala Ile Phe Ile Gly Trp Ala Gly Ser Ala Leu  
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Val Ile Leu Gly Gly Ala Leu Leu Ser Cys Ser Cys Pro Gly Asn Glu  
175 180 185 190

agc aag gct ggg tac cgt gca ccc cgc tct tac cct aag tcc aac tct 1044  
Ser Lys Ala Gly Tyr Arg Ala Pro Arg Ser Tyr Pro Lys Ser Asn Ser  
195 200 205

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Ser Lys Glu Tyr Val  
210

agtgtctaga tgcctgaaag gccctggggc tgagctcagc ctgtgggcag ggtgccggac 1159

aaaggcctcc tggtcactct gtccctgcac tccatgtata gtcctcttgg gttgggggtg 1219

gggggggtgcc gttggtggga gagacaaaaa gagggagagt gtgctttttg tacagtaata 1279

aaaaataagt attgggaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1332

&lt;210&gt; 22

&lt;211&gt; 211

&lt;212&gt; PRT

&lt;213&gt; NM\_001307 claudin 7, CLDN7

&lt;400&gt; 22

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Gly Trp Val Gly Leu Val Ala Cys Thr Ala Ile Pro Gln Trp Gln Met  
 20 25 30

Ser Ser Tyr Ala Gly Asp Asn Ile Ile Thr Ala Gln Ala Met Tyr Lys  
 35 40 45

Gly Leu Trp Met Asp Cys Val Thr Gln Ser Thr Gly Met Met Ser Cys  
 50 55 60

Lys Met Tyr Asp Ser Val Leu Ala Leu Ser Ala Ala Leu Gln Ala Thr  
 65 70 75 80

Arg Ala Leu Met Val Val Ser Leu Val Leu Gly Phe Leu Ala Met Phe  
 85 90 95

Val Ala Thr Met Gly Met Lys Cys Thr Arg Cys Gly Gly Asp Asp Lys  
 100 105 110

Val Lys Lys Ala Arg Ile Ala Met Gly Gly Gly Ile Ile Phe Ile Val  
 115 120 125

Ala Gly Leu Ala Thr Leu Val Ala Cys Ser Trp Tyr Gly His Gln Ile  
 130 135 140

Val Thr Asp Phe Tyr Asn Pro Leu Ile Pro Thr Asn Ile Lys Tyr Glu  
 145 150 155 160

Phe Gly Pro Ala Ile Phe Ile Gly Trp Ala Gly Ser Ala Leu Val Ile  
 165 170 175

Leu Gly Gly Ala Leu Leu Ser Cys Ser Cys Pro Gly Asn Glu Ser Lys  
 180 185 190

Ala Gly Tyr Arg Ala Pro Arg Ser Tyr Pro Lys Ser Asn Ser Ser Lys  
 195 200 205

Glu Tyr Val  
 210



&lt;210&gt; 23

&lt;211&gt; 888

&lt;212&gt; DNA

&lt;213&gt; NM\_014736 KIAA0101 gene product

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (75)..(407)

&lt;223&gt;

&lt;400&gt; 23

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           1             5             10

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Tyr Arg Lys Val Val Ala Ala Arg Ala Pro Arg Lys Val Leu Gly Ser
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tcc acc tct gcc act aat tcg aca tca gtt tca tcg agg aaa gct gaa      206
Ser Thr Ser Ala Thr Asn Ser Thr Ser Val Ser Ser Arg Lys Ala Glu
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aat aaa tat gca gga ggg aac ccc gtt tgc gtg cgc cca act ccc aag      254
Asn Lys Tyr Ala Gly Gly Asn Pro Val Cys Val Arg Pro Thr Pro Lys
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tgg caa aaa gga att gga gaa ttc ttt agg ttg tcc cct aaa gat tct      302
Trp Gln Lys Gly Ile Gly Glu Phe Phe Arg Leu Ser Pro Lys Asp Ser
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Glu Lys Glu Asn Gln Ile Pro Glu Glu Ala Gly Ser Ser Gly Leu Gly
           80             85             90

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Lys Ala Lys Arg Lys Ala Cys Pro Leu Gln Pro Asp His Thr Asn Asp
           95             100             105

gaa aaa gaa tagaactttc tcattcatct ttgaataacg tctccttggt      447
Glu Lys Glu
           110

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58

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888

&lt;210&gt; 24

&lt;211&gt; 111

&lt;212&gt; PRT

&lt;213&gt; NM\_014736 KIAA0101 gene product

&lt;400&gt; 24

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Val Ala Ala Arg Ala Pro Arg Lys Val Leu Gly Ser Ser Thr Ser Ala  
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Thr Asn Ser Thr Ser Val Ser Ser Arg Lys Ala Glu Asn Lys Tyr Ala  
 35 40 45

Gly Gly Asn Pro Val Cys Val Arg Pro Thr Pro Lys Trp Gln Lys Gly  
 50 55 60

Ile Gly Glu Phe Phe Arg Leu Ser Pro Lys Asp Ser Glu Lys Glu Asn  
 65 70 75 80

Gln Ile Pro Glu Glu Ala Gly Ser Ser Gly Leu Gly Lys Ala Lys Arg  
 85 90 95

Lys Ala Cys Pro Leu Gln Pro Asp His Thr Asn Asp Glu Lys Glu  
 100 105 110

&lt;210&gt; 25

&lt;211&gt; 598

&lt;212&gt; DNA

&lt;213&gt; NM\_003064 secretory leukocyte protease inhibitor, SLPI

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (23)..(418)

&lt;223&gt;

&lt;400&gt; 25

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52

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Val Leu Leu Ala Leu Gly Thr Leu Ala Pro Trp Ala Val Glu Gly Ser  
15 20 25

gga aag tcc ttc aaa gct gga gtc tgt cct cct aag aaa tct gcc cag 148  
Gly Lys Ser Phe Lys Ala Gly Val Cys Pro Pro Lys Lys Ser Ala Gln  
30 35 40

tgc ctt aga tac aag aaa cct gag tgc cag agt gac tgg cag tgt cca 196  
Cys Leu Arg Tyr Lys Lys Pro Glu Cys Gln Ser Asp Trp Gln Cys Pro  
45 50 55

ggg aag aag aga tgt tgt cct gac act tgt ggc atc aaa tgc ctg gat 244  
Gly Lys Lys Arg Cys Cys Pro Asp Thr Cys Gly Ile Lys Cys Leu Asp  
60 65 70

cct gtt gac acc cca aac cca aca agg agg aag cct ggg aag tgc cca 292  
Pro Val Asp Thr Pro Asn Pro Thr Arg Arg Lys Pro Gly Lys Cys Pro  
75 80 85 90

gtg act tat ggc caa tgt ttg atg ctt aac ccc ccc aat ttc tgt gag 340  
Val Thr Tyr Gly Gln Cys Leu Met Leu Asn Pro Pro Asn Phe Cys Glu  
95 100 105

atg gat ggc cag tgc aag cgt gac ttg aag tgt tgc atg ggc atg tgt 388  
Met Asp Gly Gln Cys Lys Arg Asp Leu Lys Cys Cys Met Gly Met Cys  
110 115 120

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Gly Lys Ser Cys Val Ser Pro Val Lys Ala  
125 130

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cactgatatc ctcccttggg gaaaggcttg gcacacagca ggctttcaag aagtgccagt 558

tgatcaatga ataaataaac gagcctatct ctctttgcac 598

&lt;210&gt; 26

&lt;211&gt; 132

&lt;212&gt; PRT

&lt;213&gt; NM\_003064 secretory leukocyte protease inhibitor, SLPI

&lt;400&gt; 26

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Thr Leu Ala Pro Trp Ala Val Glu Gly Ser Gly Lys Ser Phe Lys Ala  
20 25 30

Gly Val Cys Pro Pro Lys Lys Ser Ala Gln Cys Leu Arg Tyr Lys Lys  
35 40 45

Pro Glu Cys Gln Ser Asp Trp Gln Cys Pro Gly Lys Lys Arg Cys Cys  
50 55 60

Pro Asp Thr Cys Gly Ile Lys Cys Leu Asp Pro Val Asp Thr Pro Asn  
65 70 75 80

Pro Thr Arg Arg Lys Pro Gly Lys Cys Pro Val Thr Tyr Gly Gln Cys  
85 90 95

Leu Met Leu Asn Pro Pro Asn Phe Cys Glu Met Asp Gly Gln Cys Lys  
100 105 110

Arg Asp Leu Lys Cys Cys Met Gly Met Cys Gly Lys Ser Cys Val Ser  
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Pro Val Lys Ala  
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<210> 27

<211> 3970

<212> DNA

<213> NM\_013994 DDR1

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<221> CDS

<222> (337)..(3093)

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Lys Gly His Phe Asp Pro Ala Lys Cys Arg Tyr Ala Leu Gly Met Gln  
25 30 35  
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Asp Arg Thr Ile Pro Asp Ser Asp Ile Ser Ala Ser Ser Ser Trp Ser  
40 45 50  
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Asp 55	Ser	Thr	Ala	Ala	Arg	His	Ser	Arg	Leu	Glu	Ser	Ser	Asp	Gly	Asp 70	
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Gly	Ala	Trp	Cys	Pro	Ala	Gly	Ser	Val	Phe	Pro	Lys	Glu	Glu	Glu	Tyr	
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			90					95					100			
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Gln	Gly	Arg	His	Ala	Gly	Gly	Leu	Gly	Lys	Glu	Phe	Ser	Arg	Ser	Tyr	
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Arg	Leu	Arg	Tyr	Ser	Arg	Asp	Gly	Arg	Arg	Trp	Met	Gly	Trp	Lys	Asp	
	120					125					130					
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Arg	Trp	Gly	Gln	Glu	Val	Ile	Ser	Gly	Asn	Glu	Asp	Pro	Glu	Gly	Val	
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gtg	ctg	aag	gac	ctt	ggg	ccc	ccc	atg	gtt	gcc	cga	ctg	gtt	cgc	ttc	834
Val	Leu	Lys	Asp	Leu	Gly	Pro	Pro	Met	Val	Ala	Arg	Leu	Val	Arg	Phe	
			155					160						165		
tac	ccc	cgg	gct	gac	cgg	gtc	atg	agc	gtc	tgt	ctg	cgg	gta	gag	ctc	882
Tyr	Pro	Arg	Ala	Asp	Arg	Val	Met	Ser	Val	Cys	Leu	Arg	Val	Glu	Leu	
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tat	ggc	tgc	ctc	tgg	agg	gat	gga	ctc	ctg	tct	tac	acc	gcc	cct	gtg	930
Tyr	Gly	Cys	Leu	Trp	Arg	Asp	Gly	Leu	Leu	Ser	Tyr	Thr	Ala	Pro	Val	
		185				190						195				
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ctg	cgg	gtc	tgg	cca	ggc	tat	gac	tat	gtg	gga	tgg	agc	aac	cac	agc	1122
Leu	Arg	Val	Trp	Pro	Gly	Tyr	Asp	Tyr	Val	Gly	Trp	Ser	Asn	His	Ser	
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ttc	tcc	agt	ggc	tat	gtg	gag	atg	gag	ttt	gag	ttt	gac	cgg	ctg	agg	1170
Phe	Ser	Ser	Gly	Tyr	Val	Glu	Met	Glu	Phe	Glu	Phe	Asp	Arg	Leu	Arg	
		265				270						275				
gcc	ttc	cag	gct	atg	cag	gtc	cac	tgt	aac	aac	atg	cac	acg	ctg	gga	1218
Ala	Phe	Gln	Ala	Met	Gln	Val	His	Cys	Asn	Asn	Met	His	Thr	Leu	Gly	
	280					285					290					
gcc	cgt	ctg	cct	ggc	ggg	gtg	gaa	tgt	cgc	ttc	cgg	cgt	ggc	cct	gcc	1266
Ala	Arg	Leu	Pro	Gly	Gly	Val	Glu	Cys	Arg	Phe	Arg	Arg	Gly	Pro	Ala	
295					300					305					310	
atg	gcc	tgg	gag	ggg	gag	ccc	atg	cgc	cac	aac	cta	ggg	ggc	aac	ctg	1314
Met	Ala	Trp	Glu	Gly	Glu	Pro	Met	Arg	His	Asn	Leu	Gly	Gly	Asn	Leu	
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gca ctg gga ggc acc ttc ccg cca gcc ccc tgg tgg ccg cct ggc cca Ala Leu Gly Gly Thr Phe Pro Pro Ala Pro Trp Trp Pro Pro Gly Pro 375 380 385 390	1506
cct ccc acc aac ttc agc agc ttg gag ctg gag ccc aga ggc cag cag Pro Pro Thr Asn Phe Ser Ser Leu Glu Leu Glu Pro Arg Gly Gln Gln 395 400 405	1554
ccc gtg gcc aag gcc gag ggg agc ccg acc gcc atc ctc atc ggc tgc Pro Val Ala Lys Ala Glu Gly Ser Pro Thr Ala Ile Leu Ile Gly Cys 410 415 420	1602
ctg gtg gcc atc atc ctg ctc ctg ctg ctc atc att gcc ctc atg ctc Leu Val Ala Ile Ile Leu Leu Leu Leu Leu Ile Ile Ala Leu Met Leu 425 430 435	1650
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ttg gaa gag gag ctg acg gtt cac ctc tct gtc cct ggg gac act atc Leu Glu Glu Glu Leu Thr Val His Leu Ser Val Pro Gly Asp Thr Ile 455 460 465 470	1746
ctc atc aac aac cgc cca ggt cct aga gag cca ccc ccg tac cag gag Leu Ile Asn Asn Arg Pro Gly Pro Arg Glu Pro Pro Pro Tyr Gln Glu 475 480 485	1794
ccc cgg cct cgt ggg aat ccg ccc cac tcc gct ccc tgt gtc ccc aat Pro Arg Pro Arg Gly Asn Pro Pro His Ser Ala Pro Cys Val Pro Asn 490 495 500	1842
ggc tct gcg ttg ctg ctc tcc aat cca gcc tac cgc ctc ctt ctg gcc Gly Ser Ala Leu Leu Leu Ser Asn Pro Ala Tyr Arg Leu Leu Leu Ala 505 510 515	1890
act tac gcc cgt ccc cct cga ggc ccg ggc ccc ccc aca ccc gcc tgg Thr Tyr Ala Arg Pro Pro Arg Gly Pro Gly Pro Pro Thr Pro Ala Trp 520 525 530	1938
gcc aaa ccc acc aac acc cag gcc tac agt ggg gac tat atg gag cct Ala Lys Pro Thr Asn Thr Gln Ala Tyr Ser Gly Asp Tyr Met Glu Pro 535 540 545 550	1986
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ccc cat tat gcc gag gct gac att gtt acc ctg cag ggc gtc acc ggg Pro His Tyr Ala Glu Ala Asp Ile Val Thr Leu Gln Gly Val Thr Gly 570 575 580	2082

ggc aac acc tat gct gtg cct gca ctg ccc cca ggg gca gtc ggg gat Gly Asn Thr Tyr Ala Val Pro Ala Leu Pro Pro Gly Ala Val Gly Asp 585 590 595	2130
ggg ccc ccc aga gtg gat ttc cct cga tct cga ctc cgc ttc aag gag Gly Pro Pro Arg Val Asp Phe Pro Arg Ser Arg Leu Arg Phe Lys Glu 600 605 610	2178
aag ctt ggc gag ggc cag ttt ggg gag gtg cac ctg tgt gag gtc gac Lys Leu Gly Glu Gly Gln Phe Gly Glu Val His Leu Cys Glu Val Asp 615 620 625 630	2226
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gga cac cct ttg ctg gta gct gtc aag atc tta cgg cca gat gcc acc Gly His Pro Leu Leu Val Ala Val Lys Ile Leu Arg Pro Asp Ala Thr 650 655 660	2322
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gag aac ggc gac ctc aac cag ttc ctc agt gcc cac cag ctg gag gac Glu Asn Gly Asp Leu Asn Gln Phe Leu Ser Ala His Gln Leu Glu Asp 715 720 725	2514
aag gca gcc gag ggg gcc cct ggg gac ggg cag gct gcg cag ggg ccc Lys Ala Ala Glu Gly Ala Pro Gly Asp Gly Gln Ala Ala Gln Gly Pro 730 735 740	2562
acc atc agc tac cca atg ctg ctg cat gtg gca gcc cag atc gcc tcc Thr Ile Ser Tyr Pro Met Leu Leu His Val Ala Ala Gln Ile Ala Ser 745 750 755	2610
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acg cgg aac tgc cta gtt ggg gaa aat ttc acc atc aaa atc gca gac Thr Arg Asn Cys Leu Val Gly Glu Asn Phe Thr Ile Lys Ile Ala Asp 775 780 785 790	2706
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ggc cgg gca gtg ctg ccc atc cgc tgg atg gcc tgg gag tgc atc ctc Gly Arg Ala Val Leu Pro Ile Arg Trp Met Ala Trp Glu Cys Ile Leu 810 815 820	2802
atg ggg aag ttc acg act gcg agt gac gtg tgg gcc ttt ggt gtg acc Met Gly Lys Phe Thr Thr Ala Ser Asp Val Trp Ala Phe Gly Val Thr 825 830 835	2850
ctg tgg gag gtg ctg atg ctc tgt agg gcc cag ccc ttt ggg tca gct Leu Trp Glu Val Leu Met Leu Cys Arg Ala Gln Pro Phe Gly Ser Ala	2898

840	845	850	
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His Arg Arg Ala Gly	His Arg Glu Arg Gly	Gly Val Leu Pro Gly Pro	
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ggg ccg gca gtg tac ctg tcc cgg ccg cct gcc tgc ccg cag ggc cta			2994
Gly Pro Ala Val Tyr Leu Ser Arg Pro Pro Ala Cys Pro Gln Gly Leu			
	875	880 885	
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Tyr Glu Leu Met Tyr Leu Arg Cys Trp Ser Arg Glu Ser Glu Gln Arg Pro			
	890	895 900	
ccc ttt tcc cag ctg cat cgg ttc ctg gca gag gat gca ctc aac acg			3090
Pro Phe Ser Gln Leu His Arg Phe Leu Ala Glu Asp Ala Leu Asn Thr			
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Val			
cagtgcact aaaacaagag gacacaatgg cacctctgcc cttccctcc cgacagcca			3203
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&lt;213&gt; NM\_013994 DDR1

&lt;400&gt; 28

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Ser Gly Asp Ala Asp Met Lys Gly His Phe Asp Pro Ala Lys Cys Arg



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Ala Ser Ser Ser Trp Ser Asp Ser Thr Ala Ala Arg His Ser Arg Leu		
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Glu Ser Ser Asp Gly Asp Gly Ala Trp Cys Pro Ala Gly Ser Val Phe		
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Pro Lys Glu Glu Glu Tyr Leu Gln Val Asp Leu Gln Arg Leu His Leu		
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Val Ala Leu Val Gly Thr Gln Gly Arg His Ala Gly Gly Leu Gly Lys		
100	105	110
Glu Phe Ser Arg Ser Tyr Arg Leu Arg Tyr Ser Arg Asp Gly Arg Arg		
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Trp Met Gly Trp Lys Asp Arg Trp Gly Gln Glu Val Ile Ser Gly Asn		
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Glu Asp Pro Glu Gly Val Val Leu Lys Asp Leu Gly Pro Pro Met Val		
145	150	155
Ala Arg Leu Val Arg Phe Tyr Pro Arg Ala Asp Arg Val Met Ser Val		
165	170	175
Cys Leu Arg Val Glu Leu Tyr Gly Cys Leu Trp Arg Asp Gly Leu Leu		
180	185	190
Ser Tyr Thr Ala Pro Val Gly Gln Thr Met Tyr Leu Ser Glu Ala Val		
195	200	205
Tyr Leu Asn Asp Ser Thr Tyr Asp Gly His Thr Val Gly Gly Leu Gln		
210	215	220
Tyr Gly Gly Leu Gly Gln Leu Ala Asp Gly Val Val Gly Leu Asp Asp		
225	230	235
Phe Arg Lys Ser Gln Glu Leu Arg Val Trp Pro Gly Tyr Asp Tyr Val		
245	250	255
Gly Trp Ser Asn His Ser Phe Ser Ser Gly Tyr Val Glu Met Glu Phe		
260	265	270
Glu Phe Asp Arg Leu Arg Ala Phe Gln Ala Met Gln Val His Cys Asn		
275	280	285
Asn Met His Thr Leu Gly Ala Arg Leu Pro Gly Gly Val Glu Cys Arg		

290                      295                      300  
 Phe Arg Arg Gly Pro Ala Met Ala Trp Glu Gly Glu Pro Met Arg His  
 305                      310                      315                      320  
 Asn Leu Gly Gly Asn Leu Gly Asp Pro Arg Ala Arg Ala Val Ser Val  
 325                      330                      335  
 Pro Leu Gly Gly Arg Val Ala Arg Phe Leu Gln Cys Arg Phe Leu Phe  
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 Ala Gly Pro Trp Leu Leu Phe Ser Glu Ile Ser Phe Ile Ser Asp Val  
 355                      360                      365  
 Val Asn Asn Ser Ser Pro Ala Leu Gly Gly Thr Phe Pro Pro Ala Pro  
 370                      375                      380  
 Trp Trp Pro Pro Gly Pro Pro Pro Thr Asn Phe Ser Ser Leu Glu Leu  
 385                      390                      395                      400  
 Glu Pro Arg Gly Gln Gln Pro Val Ala Lys Ala Glu Gly Ser Pro Thr  
 405                      410                      415  
 Ala Ile Leu Ile Gly Cys Leu Val Ala Ile Ile Leu Leu Leu Leu Leu  
 420                      425                      430  
 Ile Ile Ala Leu Met Leu Trp Arg Leu His Trp Arg Arg Leu Leu Ser  
 435                      440                      445  
 Lys Ala Glu Arg Arg Val Leu Glu Glu Glu Leu Thr Val His Leu Ser  
 450                      455                      460  
 Val Pro Gly Asp Thr Ile Leu Ile Asn Asn Arg Pro Gly Pro Arg Glu  
 465                      470                      475                      480  
 Pro Pro Pro Tyr Gln Glu Pro Arg Pro Arg Gly Asn Pro Pro His Ser  
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 Ala Pro Cys Val Pro Asn Gly Ser Ala Leu Leu Leu Ser Asn Pro Ala  
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 Tyr Arg Leu Leu Leu Ala Thr Tyr Ala Arg Pro Pro Arg Gly Pro Gly  
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 Pro Pro Thr Pro Ala Trp Ala Lys Pro Thr Asn Thr Gln Ala Tyr Ser  
 530                      535                      540  
 Gly Asp Tyr Met Glu Pro Glu Lys Pro Gly Ala Pro Leu Leu Pro Pro  
 545                      550                      555                      560

Pro Pro Gln Asn Ser Val Pro His Tyr Ala Glu Ala Asp Ile Val Thr  
565 570 575

Leu Gln Gly Val Thr Gly Gly Asn Thr Tyr Ala Val Pro Ala Leu Pro  
580 585 590

Pro Gly Ala Val Gly Asp Gly Pro Pro Arg Val Asp Phe Pro Arg Ser  
595 600 605

Arg Leu Arg Phe Lys Glu Lys Leu Gly Glu Gly Gln Phe Gly Glu Val  
610 615 620

His Leu Cys Glu Val Asp Ser Pro Gln Asp Leu Val Ser Leu Asp Phe  
625 630 635 640

Pro Leu Asn Val Arg Lys Gly His Pro Leu Leu Val Ala Val Lys Ile  
645 650 655

Leu Arg Pro Asp Ala Thr Lys Asn Ala Ser Phe Ser Leu Phe Ser Arg  
660 665 670

Asn Asp Phe Leu Lys Glu Val Lys Ile Met Ser Arg Leu Lys Asp Pro  
675 680 685

Asn Ile Ile Arg Leu Leu Gly Val Cys Val Gln Asp Asp Pro Leu Cys  
690 695 700

Met Ile Thr Asp Tyr Met Glu Asn Gly Asp Leu Asn Gln Phe Leu Ser  
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Ala His Gln Leu Glu Asp Lys Ala Ala Glu Gly Ala Pro Gly Asp Gly  
725 730 735

Gln Ala Ala Gln Gly Pro Thr Ile Ser Tyr Pro Met Leu Leu His Val  
740 745 750

Ala Ala Gln Ile Ala Ser Gly Met Arg Tyr Leu Ala Thr Leu Asn Phe  
755 760 765

Val His Arg Asp Leu Ala Thr Arg Asn Cys Leu Val Gly Glu Asn Phe  
770 775 780

Thr Ile Lys Ile Ala Asp Phe Gly Met Ser Arg Asn Leu Tyr Ala Gly  
785 790 795 800

Asp Tyr Tyr Arg Val Gln Gly Arg Ala Val Leu Pro Ile Arg Trp Met  
805 810 815

Ala Trp Glu Cys Ile Leu Met Gly Lys Phe Thr Thr Ala Ser Asp Val  
820 825 830

Trp Ala Phe Gly Val Thr Leu Trp Glu Val Leu Met Leu Cys Arg Ala  
835 840 845

Gln Pro Phe Gly Ser Ala His Arg Arg Ala Gly His Arg Glu Arg Gly  
850 855 860

Gly Val Leu Pro Gly Pro Gly Pro Ala Val Tyr Leu Ser Arg Pro Pro  
865 870 875 880

Ala Cys Pro Gln Gly Leu Tyr Glu Leu Met Leu Arg Cys Trp Ser Arg  
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tggctctcgtg gggtcctgcc tggttagtcg ctttcagggt tcttgagccc cttcagcacc 120

gtcacc atg gaa gtg tca cca ttg cag cct gta aat gaa aat atg caa 168  
Met Glu Val Ser Pro Leu Gln Pro Val Asn Glu Asn Met Gln  
1 5 10

gtc aac aaa ata aag aaa aat gaa gat gct aag aaa aga ctg tct gtt 216  
Val Asn Lys Ile Lys Lys Asn Glu Asp Ala Lys Lys Arg Leu Ser Val  
15 20 25 30

gaa aga atc tat caa aag aaa aca caa ttg gaa cat att ttg ctc cgc 264  
Glu Arg Ile Tyr Gln Lys Lys Thr Gln Leu Glu His Ile Leu Leu Arg  
35 40 45

cca gac acc tac att ggt tct gtg gaa tta gtg acc cag caa atg tgg 312  
Pro Asp Thr Tyr Ile Gly Ser Val Glu Leu Val Thr Gln Gln Met Trp  
50 55 60

gtt tac gat gaa gat gtt ggc att aac tat agg gaa gtc act ttt gtt 360

Val	Tyr	Asp	Glu	Asp	Val	Gly	Ile	Asn	Tyr	Arg	Glu	Val	Thr	Phe	Val	
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Pro	Gly	Leu	Tyr	Lys	Ile	Phe	Asp	Glu	Ile	Leu	Val	Asn	Ala	Ala	Asp	
	80					85					90					
aac	aaa	caa	agg	gac	cca	aaa	atg	tct	tgt	att	aga	gtc	aca	att	gat	456
Asn	Lys	Gln	Arg	Asp	Pro	Lys	Met	Ser	Cys	Ile	Arg	Val	Thr	Ile	Asp	
	95				100					105					110	
ccg	gaa	aac	aat	tta	att	agt	ata	tgg	aat	aat	gga	aaa	ggt	att	cct	504
Pro	Glu	Asn	Asn	Leu	Ile	Ser	Ile	Trp	Asn	Asn	Gly	Lys	Gly	Ile	Pro	
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gtt	gtt	gaa	cac	aaa	gtt	gaa	aag	atg	tat	gtc	cca	gct	ctc	ata	ttt	552
Val	Val	Glu	His	Lys	Val	Glu	Lys	Met	Tyr	Val	Pro	Ala	Leu	Ile	Phe	
			130					135					140			
gga	cag	ctc	cta	act	tct	agt	aac	tat	gat	gat	gat	gaa	aag	aaa	gtg	600
Gly	Gln	Leu	Leu	Thr	Ser	Ser	Asn	Tyr	Asp	Asp	Asp	Glu	Lys	Lys	Val	
		145					150					155				
aca	ggt	ggt	cga	aat	ggc	tat	gga	gcc	aaa	ttg	tgt	aac	ata	ttc	agt	648
Thr	Gly	Gly	Arg	Asn	Gly	Tyr	Gly	Ala	Lys	Leu	Cys	Asn	Ile	Phe	Ser	
	160					165					170					
acc	aaa	ttt	act	gtg	gaa	aca	gcc	agt	aga	gaa	tac	aag	aaa	atg	ttc	696
Thr	Lys	Phe	Thr	Val	Glu	Thr	Ala	Ser	Arg	Glu	Tyr	Lys	Lys	Met	Phe	
	175				180					185					190	
aaa	cag	aca	tgg	atg	gat	aat	atg	gga	aga	gct	ggt	gag	atg	gaa	ctc	744
Lys	Gln	Thr	Trp	Met	Asp	Asn	Met	Gly	Arg	Ala	Gly	Glu	Met	Glu	Leu	
				195				200						205		
aag	ccc	ttc	aat	gga	gaa	gat	tat	aca	tgt	atc	acc	ttt	cag	cct	gat	792
Lys	Pro	Phe	Asn	Gly	Glu	Asp	Tyr	Thr	Cys	Ile	Thr	Phe	Gln	Pro	Asp	
			210					215					220			
ttg	tct	aag	ttt	aaa	atg	caa	agc	ctg	gac	aaa	gat	att	gtt	gca	cta	840
Leu	Ser	Lys	Phe	Lys	Met	Gln	Ser	Leu	Asp	Lys	Asp	Ile	Val	Ala	Leu	
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atg	gtc	aga	aga	gca	tat	gat	att	gct	gga	tcc	acc	aaa	gat	gtc	aaa	888
Met	Val	Arg	Arg	Ala	Tyr	Asp	Ile	Ala	Gly	Ser	Thr	Lys	Asp	Val	Lys	
	240					245				250						
gtc	ttt	ctt	aat	gga	aat	aaa	ctg	cca	gta	aaa	gga	ttt	cgt	agt	tat	936
Val	Phe	Leu	Asn	Gly	Asn	Lys	Leu	Pro	Val	Lys	Gly	Phe	Arg	Ser	Tyr	
	255				260					265					270	
gtg	gac	atg	tat	ttg	aag	gac	aag	ttg	gat	gaa	act	ggt	aac	tcc	ttg	984
Val	Asp	Met	Tyr	Leu	Lys	Asp	Lys	Leu	Asp	Glu	Thr	Gly	Asn	Ser	Leu	
				275					280					285		
aaa	gta	ata	cat	gaa	caa	gta	aac	cac	agg	tgg	gaa	gtg	tgt	tta	act	1032
Lys	Val	Ile	His	Glu	Gln	Val	Asn	His	Arg	Trp	Glu	Val	Cys	Leu	Thr	
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Thr	Ser	Lys	Gly	Gly	Arg	His	Val	Asp	Tyr	Val	Ala	Asp	Gln	Ile	Val	
		320				325					330					

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gta aaa gca cat cag gtg aaa aat cac atg tgg att ttt gta aat gcc Val Lys Ala His Gln Val Lys Asn His Met Trp Ile Phe Val Asn Ala 355 360 365	1224
tta att gaa aac cca acc ttt gac tct cag aca aaa gaa aac atg act Leu Ile Glu Asn Pro Thr Phe Asp Ser Gln Thr Lys Glu Asn Met Thr 370 375 380	1272
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gac caa gat ggt tcc cac atc aaa ggc ttg ctg att aat ttt atc cat Asp Gln Asp Gly Ser His Ile Lys Gly Leu Leu Ile Asn Phe Ile His 545 550 555	1800
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act ccc att gta aag gta tct aaa aac aag caa gaa atg gca ttt tac Thr Pro Ile Val Lys Val Ser Lys Asn Lys Gln Glu Met Ala Phe Tyr 575 580 585 590	1896
agc ctt cct gaa ttt gaa gag tgg aag agt tct act cca aat cat aaa	1944

Ser	Leu	Pro	Glu	Phe	Glu	Glu	Trp	Lys	Ser	Ser	Thr	Pro	Asn	His	Lys	
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aaa	tgg	aaa	gtc	aaa	tat	tac	aaa	ggg	ttg	ggc	acc	agc	aca	tca	aag	1992
Lys	Trp	Lys	Val	Lys	Tyr	Tyr	Lys	Gly	Leu	Gly	Thr	Ser	Thr	Ser	Lys	
			610					615					620			
gaa	gct	aaa	gaa	tac	ttt	gca	gat	atg	aaa	aga	cat	cgt	atc	cag	ttc	2040
Glu	Ala	Lys	Glu	Tyr	Phe	Ala	Asp	Met	Lys	Arg	His	Arg	Ile	Gln	Phe	
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aaa	tat	tct	ggg	cct	gaa	gat	gat	gct	gct	atc	agc	ctg	gcc	ttt	agc	2088
Lys	Tyr	Ser	Gly	Pro	Glu	Asp	Asp	Ala	Ala	Ile	Ser	Leu	Ala	Phe	Ser	
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aaa	aaa	cag	ata	gat	gat	cga	aag	gaa	tgg	tta	act	aat	ttc	atg	gag	2136
Lys	Lys	Gln	Ile	Asp	Arg	Arg	Lys	Glu	Trp	Leu	Thr	Asn	Phe	Met	Glu	
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gat	aga	aga	caa	cga	aag	tta	ctt	ggg	ctt	cct	gag	gat	tac	ttg	tat	2184
Asp	Arg	Arg	Gln	Arg	Lys	Leu	Leu	Gly	Leu	Pro	Glu	Asp	Tyr	Leu	Tyr	
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gga	caa	act	acc	aca	tat	ctg	aca	tat	aat	gac	ttc	atc	aac	aag	gaa	2232
Gly	Gln	Thr	Thr	Thr	Tyr	Leu	Thr	Tyr	Asn	Asp	Phe	Ile	Asn	Lys	Glu	
				690				695					700			
ctt	atc	ttg	ttc	tca	aat	tct	gat	aac	gag	aga	tct	atc	cct	tct	atg	2280
Leu	Ile	Leu	Phe	Ser	Asn	Ser	Asp	Asn	Glu	Arg	Ser	Ile	Pro	Ser	Met	
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gtg	gat	ggg	ttg	aaa	cca	ggg	cag	aga	aag	gtt	ttg	ttt	act	tgc	ttc	2328
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Lys	Arg	Asn	Asp	Lys	Arg	Glu	Val	Lys	Val	Ala	Gln	Leu	Ala	Gly	Ser	
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gtg	gct	gaa	atg	tct	tct	tat	cat	cat	ggg	gag	atg	tca	cta	atg	atg	2424
Val	Ala	Glu	Met	Ser	Ser	Tyr	His	His	Gly	Glu	Met	Ser	Leu	Met	Met	
				755					760					765		
acc	att	atc	aat	ttg	gct	cag	aat	ttt	gtg	ggg	agc	aat	aat	cta	aac	2472
Thr	Ile	Ile	Asn	Leu	Ala	Gln	Asn	Phe	Val	Gly	Ser	Asn	Asn	Leu	Asn	
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Thr Thr Thr Tyr Leu Thr Tyr Asn Asp Phe Ile Asn Lys Glu Leu Ile  
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gtatctggcc cctgggcagc tgcccgggga ggcggccagc gagctggggc cgcgca atg      239
                                         Met
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Ser His Gly Ala Gly Leu Val Arg Thr Thr Cys Ser Ser Gly Ser Ala
           5                      10                      15

ctc gga ccc ggg gcc ggc gcg gcc cag ccc agc gcg agc ccc ttg gag      335
Leu Gly Pro Gly Ala Gly Ala Ala Gln Pro Ser Ala Ser Pro Leu Glu
           20                      25                      30

ggg ctg ctg gac ctc agc tac ccc cgc acc cac gcg gcc ctg ctg aaa      383
Gly Leu Leu Asp Leu Ser Tyr Pro Arg Thr His Ala Ala Leu Leu Lys
           35                      40                      45

gtg gcg caa atg gtc acc ctg ctg att gcc ttc atc tgt gtg cgg agc      431
Val Ala Gln Met Val Thr Leu Leu Ile Ala Phe Ile Cys Val Arg Ser
           50                      55                      60                      65

tcc ctg tgg acc aac tac agc gcc tac agc tac ttt gaa gtg gtc acc      479
Ser Leu Trp Thr Asn Tyr Ser Ala Tyr Ser Tyr Phe Glu Val Val Thr
           70                      75                      80

att tgc gac ttg ata atg atc ctc gcc ttt tac ctg gtc cac ctc ttc      527
Ile Cys Asp Leu Ile Met Ile Leu Ala Phe Tyr Leu Val His Leu Phe
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cgc ttc tac cgc gtg ctc acc tgt atc agc tgg ccc ctg tcg gaa ctt      575

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Arg Phe Tyr Arg Val Leu Thr Cys Ile Ser Trp Pro Leu Ser Glu Leu  
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 Leu His Tyr Leu Ile Gly Thr Leu Leu Leu Leu Ile Ala Ser Ile Val  
 115 120 125

gca gct tcc aag agt tac aac cag agc gga ctg gta gcc gga gcg atc 671  
 Ala Ala Ser Lys Ser Tyr Asn Gln Ser Gly Leu Val Ala Gly Ala Ile  
 130 135 140 145

ttt ggt ttc atg gcc acc ttc ctc tgc atg gca agc ata tgg ctg tcc 719  
 Phe Gly Phe Met Ala Thr Phe Leu Cys Met Ala Ser Ile Trp Leu Ser  
 150 155 160

tat aag atc tcg tgt gta acc cag tcc aca gat gca gcc gtc 761  
 Tyr Lys Ile Ser Cys Val Thr Gln Ser Thr Asp Ala Ala Val  
 165 170 175

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gccggaaact cttcctccag ccttccgggg agaacatccc tcccattctg ggaaaggaaa 1001

gcagcctcca gggaaatggt ttctgccttc ctgcttctag aaccacctca ggtactgatg 1061

aaccccaact agcacagctg aagggtttg tgaatactcc cgcctaaatc ccttctactt 1121

cactcctcag gggagtgaag tgccttaaga aacaaagccc tgtcctaatt tatctagctt 1181

gtcagtcagg tcttagagat accctctttc ctgaagttag gcgtgcctgt agaaacacta 1241

tgtggtcagc ctgtccocaa ggagatcttg tgtctcctct ccatctctgc ctttggtacc 1301

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Glu Gly Leu Leu Asp Leu Ser Tyr Pro Arg Thr His Ala Ala Leu Leu  
 35 40 45

Lys Val Ala Gln Met Val Thr Leu Leu Ile Ala Phe Ile Cys Val Arg  
 50 55 60

Ser Ser Leu Trp Thr Asn Tyr Ser Ala Tyr Ser Tyr Phe Glu Val Val  
65 70 75 80

Thr Ile Cys Asp Leu Ile Met Ile Leu Ala Phe Tyr Leu Val His Leu  
85 90 95

Phe Arg Phe Tyr Arg Val Leu Thr Cys Ile Ser Trp Pro Leu Ser Glu  
100 105 110

Leu Leu His Tyr Leu Ile Gly Thr Leu Leu Leu Leu Ile Ala Ser Ile  
115 120 125

Val Ala Ala Ser Lys Ser Tyr Asn Gln Ser Gly Leu Val Ala Gly Ala  
130 135 140

Ile Phe Gly Phe Met Ala Thr Phe Leu Cys Met Ala Ser Ile Trp Leu  
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Ser Tyr Lys Ile Ser Cys Val Thr Gln Ser Thr Asp Ala Ala Val  
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tggcttctga ggcggttgcg gtgctcggtc gccgcctagg cggggcaggg tgcgagcagg 180  
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agacttcaag atttcagaaa aggggtgaaa gagaagattg caactttgag tcagacctgt 360  
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tgggaaaaac ctgctcttct gcgttaagtg ggagaca atg tca caa gtt aaa agc 475  
Met Ser Gln Val Lys Ser  
1 5

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gat gat gaa gga gat act caa aac ata gat tca tgg ttt gag gag aag Asp Asp Glu Gly Asp Thr Gln Asn Ile Asp Ser Trp Phe Glu Glu Lys 25 30 35	571
gcc aat ttg gag aat aag tta ctg ggg aag aat gga act gga ggg ctt Ala Asn Leu Glu Asn Lys Leu Leu Gly Lys Asn Gly Thr Gly Gly Leu 40 45 50	619
ttt cag ggc aaa act cct ttg aga aag gct aat ctt cag caa gct att Phe Gln Gly Lys Thr Pro Leu Arg Lys Ala Asn Leu Gln Gln Ala Ile 55 60 65 70	667
gtc aca cct ttg aaa cca gtt gac aac act tac tac aaa gag gca gaa Val Thr Pro Leu Lys Pro Val Asp Asn Thr Tyr Tyr Lys Glu Ala Glu 75 80 85	715
aaa gaa aat ctt gtg gaa caa tcc att ccg tca aat gct tgt tct tcc Lys Glu Asn Leu Val Glu Gln Ser Ile Pro Ser Asn Ala Cys Ser Ser 90 95 100	763
ctg gaa gtt gag gca gcc ata tca aga aaa act cca gcc cag cct cag Leu Glu Val Glu Ala Ala Ile Ser Arg Lys Thr Pro Ala Gln Pro Gln 105 110 115	811
aga aga tct ctt agg ctt tct gct cag aag gat ttg gaa cag aaa gaa Arg Arg Ser Leu Arg Leu Ser Ala Gln Lys Asp Leu Glu Gln Lys Glu 120 125 130	859
aag cat cat gta aaa atg aaa gcc aag aga tgt gcc act cct gta atc Lys His His Val Lys Met Lys Ala Lys Arg Cys Ala Thr Pro Val Ile 135 140 145 150	907
atc gat gaa att cta ccc tct aag aaa atg aaa gtt tct aac aac aaa Ile Asp Glu Ile Leu Pro Ser Lys Lys Met Lys Val Ser Asn Asn Lys 155 160 165	955
aag aag cca gag gaa gaa ggc agt gct cat caa gat act gct gaa aag Lys Lys Pro Glu Glu Glu Gly Ser Ala His Gln Asp Thr Ala Glu Lys 170 175 180	1003
aat gca tct tcc cca gag aaa gcc aag ggt aga cat act gtg cct tgt Asn Ala Ser Ser Pro Glu Lys Ala Lys Gly Arg His Thr Val Pro Cys 185 190 195	1051
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ctg gag aag agt atg aaa atg cag caa gag gtg gtg gag atg cgg aaa Leu Glu Lys Ser Met Lys Met Gln Gln Glu Val Val Glu Met Arg Lys 215 220 225 230	1147
aag aat gaa gaa ttc aag aaa ctt gct ctg gct gga ata ggg caa cct Lys Asn Glu Glu Phe Lys Lys Leu Ala Leu Ala Gly Ile Gly Gln Pro 235 240 245	1195
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cgc aca gat gag cga atc aaa caa cat cct aag aac cag gag gaa tat Arg Thr Asp Glu Arg Ile Lys Gln His Pro Lys Asn Gln Glu Glu Tyr 265 270 275	1291

aag gaa gtg aac ttt aca tct gaa cta cga aag cat cct tca tct cct Lys Glu Val Asn Phe Thr Ser Glu Leu Arg Lys His Pro Ser Ser Pro 280 285 290	1339
gcc cga gtg act aag gga tgt acc att gtt aag cct ttc aac ctg tcc Ala Arg Val Thr Lys Gly Cys Thr Ile Val Lys Pro Phe Asn Leu Ser 295 300 305 310	1387
caa gga aag aaa aga aca ttt gat gaa aca gtt tct aca tat gtg ccc Gln Gly Lys Lys Arg Thr Phe Asp Glu Thr Val Ser Thr Tyr Val Pro 315 320 325	1435
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cat ttg agg agc aag aag gat gat att aac ctg tta ccc tcc aaa tct His Leu Arg Ser Lys Lys Asp Asp Ile Asn Leu Leu Pro Ser Lys Ser 345 350 355	1531
tct gtg acc aag att tgc aga gac cca cag act cct gta ctg caa acc Ser Val Thr Lys Ile Cys Arg Asp Pro Gln Thr Pro Val Leu Gln Thr 360 365 370	1579
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gct gag gag ctc gag aaa ttg caa caa tac aaa ttc aaa gca cgt gaa Ala Glu Glu Leu Glu Lys Leu Gln Gln Tyr Lys Phe Lys Ala Arg Glu 395 400 405	1675
ctt gat ccc aga ata ctt gaa ggt ggg ccc atc ttg ccc aag aaa cca Leu Asp Pro Arg Ile Leu Glu Gly Gly Pro Ile Leu Pro Lys Lys Pro 410 415 420	1723
cct gtg aaa cca ccc acc gag cct att ggc ttt gat ttg gaa att gag Pro Val Lys Pro Pro Thr Glu Pro Ile Gly Phe Asp Leu Glu Ile Glu 425 430 435	1771
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cca gcc ttt gca ttg aag aac aga att cga atg ccc acc aaa gaa gat Pro Ala Phe Ala Leu Lys Asn Arg Ile Arg Met Pro Thr Lys Glu Asp 490 495 500	1963
gag gaa gag gac gaa ccg gta gtg ata aaa gct caa cct gtg cca cat Glu Glu Glu Asp Glu Pro Val Val Ile Lys Ala Gln Pro Val Pro His 505 510 515	2011
tat ggg gtg cct ttt aag ccc caa atc cca gag gca aga act gtg gaa Tyr Gly Val Pro Phe Lys Pro Gln Ile Pro Glu Ala Arg Thr Val Glu 520 525 530	2059
ata tgc cct ttc tcg ttt gat tct cga gac aaa gaa cgt cag tta cag Ile Cys Pro Phe Ser Phe Asp Ser Arg Asp Lys Glu Arg Gln Leu Gln 535 540 545 550	2107

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gtt gct gag ggc ctt tct ggt tct cta gtt cag gaa cct ttt cag ctg Val Ala Glu Gly Leu Ser Gly Ser Leu Val Gln Glu Pro Phe Gln Leu 650 655 660	2443
gct act gag aag aga gcc aaa gag cgg cag gag ctg gag aag aga atg Ala Thr Glu Lys Arg Ala Lys Glu Arg Gln Glu Leu Glu Lys Arg Met 665 670 675	2491
gct gag gta gaa gcc cag aaa gcc cag cag ttg gag gag gcc aga cta Ala Glu Val Glu Ala Gln Lys Ala Gln Gln Leu Glu Glu Ala Arg Leu 680 685 690	2539
cag gag gaa gag cag aaa aaa gag gag ctg gcc agg cta cgg aga gaa Gln Glu Glu Glu Gln Lys Lys Glu Glu Leu Ala Arg Leu Arg Arg Glu 695 700 705 710	2587
ctg gtg cat aag gca aat cca ata cgc aag tac cag ggt ctg gag ata Leu Val His Lys Ala Asn Pro Ile Arg Lys Tyr Gln Gly Leu Glu Ile 715 720 725	2635
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Asn Gly Thr Gly Gly Leu Phe Gln Gly Lys Thr Pro Leu Arg Lys Ala  
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Asn Leu Gln Gln Ala Ile Val Thr Pro Leu Lys Pro Val Asp Asn Thr  
65 70 75 80

Tyr Tyr Lys Glu Ala Glu Lys Glu Asn Leu Val Glu Gln Ser Ile Pro  
85 90 95

Ser Asn Ala Cys Ser Ser Leu Glu Val Glu Ala Ala Ile Ser Arg Lys  
100 105 110

Thr Pro Ala Gln Pro Gln Arg Arg Ser Leu Arg Leu Ser Ala Gln Lys  
115 120 125

Asp Leu Glu Gln Lys Glu Lys His His Val Lys Met Lys Ala Lys Arg  
130 135 140

Cys Ala Thr Pro Val Ile Ile Asp Glu Ile Leu Pro Ser Lys Lys Met  
145 150 155 160

Lys Val Ser Asn Asn Lys Lys Lys Pro Glu Glu Glu Gly Ser Ala His  
165 170 175

Gln Asp Thr Ala Glu Lys Asn Ala Ser Ser Pro Glu Lys Ala Lys Gly  
 180 185 190

Arg His Thr Val Pro Cys Met Pro Pro Ala Lys Gln Lys Phe Leu Lys  
 195 200 205

Ser Thr Glu Glu Gln Glu Leu Glu Lys Ser Met Lys Met Gln Gln Glu  
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Val Val Glu Met Arg Lys Lys Asn Glu Glu Phe Lys Lys Leu Ala Leu  
 225 230 235 240

Ala Gly Ile Gly Gln Pro Val Lys Lys Ser Val Ser Gln Val Thr Lys  
 245 250 255

Ser Val Asp Phe His Phe Arg Thr Asp Glu Arg Ile Lys Gln His Pro  
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Lys Asn Gln Glu Glu Tyr Lys Glu Val Asn Phe Thr Ser Glu Leu Arg  
 275 280 285

Lys His Pro Ser Ser Pro Ala Arg Val Thr Lys Gly Cys Thr Ile Val  
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Lys Pro Phe Asn Leu Ser Gln Gly Lys Lys Arg Thr Phe Asp Glu Thr  
 305 310 315 320

Val Ser Thr Tyr Val Pro Leu Ala Gln Gln Val Glu Asp Phe His Lys  
 325 330 335

Arg Thr Pro Asn Arg Tyr His Leu Arg Ser Lys Lys Asp Asp Ile Asn  
 340 345 350

Leu Leu Pro Ser Lys Ser Ser Val Thr Lys Ile Cys Arg Asp Pro Gln  
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Thr Pro Val Leu Gln Thr Lys His Arg Ala Arg Ala Val Thr Cys Lys  
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Ser Thr Ala Glu Leu Glu Ala Glu Glu Leu Glu Lys Leu Gln Gln Tyr  
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Lys Phe Lys Ala Arg Glu Leu Asp Pro Arg Ile Leu Glu Gly Gly Pro  
 405 410 415

Ile Leu Pro Lys Lys Pro Pro Val Lys Pro Pro Thr Glu Pro Ile Gly  
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Phe Asp Leu Glu Ile Glu Lys Arg Ile Gln Glu Arg Glu Ser Lys Lys  
 435 440 445



Lys Thr Glu Asp Glu His Phe Glu Phe His Ser Arg Pro Cys Pro Thr  
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 465 470 475 480  
 Ile Thr Val Pro Lys Ser Pro Ala Phe Ala Leu Lys Asn Arg Ile Arg  
 485 490 495  
 Met Pro Thr Lys Glu Asp Glu Glu Glu Asp Glu Pro Val Val Ile Lys  
 500 505 510  
 Ala Gln Pro Val Pro His Tyr Gly Val Pro Phe Lys Pro Gln Ile Pro  
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 Glu Ala Arg Thr Val Glu Ile Cys Pro Phe Ser Phe Asp Ser Arg Asp  
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 Lys Glu Arg Gln Leu Gln Lys Glu Lys Lys Ile Lys Glu Leu Gln Lys  
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 Ile Asn Leu Pro Glu Lys Lys Val Lys Asn Val Thr Gln Ile Glu Pro  
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 Lys His Gln Leu Glu Glu Glu Leu Arg Gln Gln Lys Glu Ala Ala Cys  
 610 615 620  
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 625 630 635 640  
 Lys Lys Glu Lys Lys Ser Val Ala Glu Gly Leu Ser Gly Ser Leu Val  
 645 650 655  
 Gln Glu Pro Phe Gln Leu Ala Thr Glu Lys Arg Ala Lys Glu Arg Gln  
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 Glu Leu Glu Lys Arg Met Ala Glu Val Glu Ala Gln Lys Ala Gln Gln  
 675 680 685  
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 690 695 700  
 Ala Arg Leu Arg Arg Glu Leu Val His Lys Ala Asn Pro Ile Arg Lys  
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gtc aaa gga ggc acc aag tgc atc aaa tac ctg ctg ttc gga ttt aac 165  
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 Phe Ile Phe Trp Leu Ala Gly Ile Ala Val Leu Ala Ile Gly Leu Trp  
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ctc cga ttc gac tct cag acc aag agc atc ttc gag caa gaa act aat 261  
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 35 40 45 50

aat aat aat tcc agc ttc tac aca gga gtc tat att ctg atc gga gcc 309  
 Asn Asn Asn Ser Ser Phe Tyr Thr Gly Val Tyr Ile Leu Ile Gly Ala  
 55 60 65

ggc gcc ctc atg atg ctg gtg ggc ttc ctg ggc tgc tgc ggg gct gtg 357  
 Gly Ala Leu Met Met Leu Val Gly Phe Leu Gly Cys Cys Gly Ala Val  
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 Ile Phe Ala Ile Glu Ile Ala Ala Ala Ile Trp Gly Tyr Ser His Lys  
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gat gag gtg att aag gaa gtc cag gag ttt tac aag gac acc tac aac 501  
 Asp Glu Val Ile Lys Glu Val Gln Glu Phe Tyr Lys Asp Thr Tyr Asn  
 115 120 125 130

aag ctg aaa acc aag gat gag ccc cag cgg gaa acg ctg aaa gcc atc 549

Lys Leu Lys Thr Lys Asp Glu Pro Gln Arg Glu Thr Leu Lys Ala Ile  
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 His Tyr Ala Leu Asn Cys Cys Gly Leu Ala Gly Gly Val Glu Gln Phe  
 150 155 160  
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 Ile Ser Asp Ile Cys Pro Lys Lys Asp Val Leu Glu Thr Phe Thr Val  
 165 170 175  
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 Lys Ser Cys Pro Asp Ala Ile Lys Glu Val Phe Asp Asn Lys Phe His  
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 Leu Trp Leu Arg Phe Asp Ser Gln Thr Lys Ser Ile Phe Glu Gln Glu  
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 Thr Asn Asn Asn Asn Ser Ser Phe Tyr Thr Gly Val Tyr Ile Leu Ile  
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Gly Ala Gly Ala Leu Met Met Leu Val Gly Phe Leu Gly Cys Cys Gly  
65 70 75 80

Ala Val Gln Glu Ser Gln Cys Met Leu Gly Leu Phe Phe Gly Phe Leu  
85 90 95

Leu Val Ile Phe Ala Ile Glu Ile Ala Ala Ala Ile Trp Gly Tyr Ser  
100 105 110

His Lys Asp Glu Val Ile Lys Glu Val Gln Glu Phe Tyr Lys Asp Thr  
115 120 125

Tyr Asn Lys Leu Lys Thr Lys Asp Glu Pro Gln Arg Glu Thr Leu Lys  
130 135 140

Ala Ile His Tyr Ala Leu Asn Cys Cys Gly Leu Ala Gly Gly Val Glu  
145 150 155 160

Gln Phe Ile Ser Asp Ile Cys Pro Lys Lys Asp Val Leu Glu Thr Phe  
165 170 175

Thr Val Lys Ser Cys Pro Asp Ala Ile Lys Glu Val Phe Asp Asn Lys  
180 185 190

Phe His Ile Ile Gly Ala Val Gly Ile Gly Ile Ala Val Val Met Ile  
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Arg Glu Met Val  
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taacttcctt actctttctc tcaagaggag gcaagtggct gtggcgggcg cagcagtggc	180
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cctaagaaac aaactatgaa ctgattgttg aaaaaagaa gtaaaaagt ttagcacagc	360
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ggaagttttg acgaacggag tagagatgta taccacttgg gggcttcagt gagaaccag	720
aattcctgga ggaggattta cattcagaaa tgttgaagtg aaaattcctt ctgggttcagc	780
atcttgaggt tcagcttgga agaacatttt acgtatggaa gaatttgctt ctccaaacct	840
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gcctgagttt gcttcaggca ttttaaattt aacttgaggg atcatgtgtt tggcatg	957
atg agg acc act gaa gac ttc cac aag cct agt gcc aca tta aac tct	1005
Met Arg Thr Thr Glu Asp Phe His Lys Pro Ser Ala Thr Leu Asn Ser	
1 5 10 15	
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Asn Thr Ala Thr Lys Gly Arg Tyr Ile Tyr Leu Glu Ala Phe Leu Glu	
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Gly Gly Ala Pro Trp Gly Phe Thr Leu Lys Gly Gly Leu Glu His Gly	
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Glu Pro Leu Ile Ile Ser Lys Val Glu Glu Gly Gly Lys Ala Asp Thr	
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Leu Ser Ser Lys Leu Gln Ala Gly Asp Glu Val Val His Ile Asn Glu	
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gtg act ctg agc agc tcc aga aag gag gca gtt tcc ctg gtg aaa gga	1245
Val Thr Leu Ser Ser Ser Arg Lys Glu Ala Val Ser Leu Val Lys Gly	
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Ser Tyr Lys Thr Leu Arg Leu Val Val Arg Arg Asp Val Cys Thr Asp	
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cca ggc cat gca gat act ggt gcc tct aac ttc gtc agc cca gaa cac	1341
Pro Gly His Ala Asp Thr Gly Ala Ser Asn Phe Val Ser Pro Glu His	
115 120 125	
ctc acc tot ggc ccc cag cac agg aaa gca gcg tgg tca gga ggg gtt	1389
Leu Thr Ser Gly Pro Gln His Arg Lys Ala Ala Trp Ser Gly Gly Val	
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aaa ctt cgg ctg aag cac agg tct agt gag cct gca ggc cga cct cac	1437

Lys 145	Leu	Arg	Leu	Lys 150	His	Arg	Ser	Ser	Glu	Pro 155	Ala	Gly	Arg	Pro	His 160	
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Ser	Trp	His	Thr	Thr	Lys	Ser	Gly	Glu	Lys	Gln	Pro	Asp	Ala	Ser	Met	
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atg	cag	ata	tct	cag	ggt	atg	atc	ggc	cct	cct	tg	cac	caa	agc	tac	1533
Met	Gln	Ile	Ser	Gln	Gly	Met	Ile	Gly	Pro	Pro	Trp	His	Gln	Ser	Tyr	
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cat	tcc	agc	tcc	tct	act	agt	gac	ctc	tcc	aac	tat	gac	cat	gct	tat	1581
His	Ser	Ser	Ser	Ser	Thr	Ser	Asp	Leu	Ser	Asn	Tyr	Asp	His	Ala	Tyr	
				195				200						205		
cta	agg	cgg	agc	cct	gac	cag	tgc	agc	tcc	cag	ggg	agc	atg	gag	agc	1629
Leu	Arg	Arg	Ser	Pro	Asp	Gln	Cys	Ser	Ser	Gln	Gly	Ser	Met	Glu	Ser	
				210				215						220		
ctg	gag	ccc	agt	ggg	gca	tac	cca	ccc	tgt	cat	ctt	tcc	cct	gcc	aag	1677
Leu	Glu	Pro	Ser	Gly	Ala	Tyr	Pro	Pro	Cys	His	Leu	Ser	Pro	Ala	Lys	
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tcc	acc	ggc	agc	att	gac	cag	ctc	agc	cac	ttc	cat	aac	aag	aga	gac	1725
Ser	Thr	Gly	Ser	Ile	Asp	Gln	Leu	Ser	His	Phe	His	Asn	Lys	Arg	Asp	
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tcg	gct	tac	agc	tct	ttc	tcc	acc	agt	tct	agc	atc	cta	gag	tat	cca	1773
Ser	Ala	Tyr	Ser	Ser	Phe	Ser	Thr	Ser	Ser	Ser	Ile	Leu	Glu	Tyr	Pro	
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cac	cct	ggc	atc	tct	gcc	cgg	gag	cgt	tca	ggc	tcc	atg	gac	aat	act	1821
His	Pro	Gly	Ile	Ser	Ala	Arg	Glu	Arg	Ser	Gly	Ser	Met	Asp	Asn	Thr	
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tct	gct	cga	ggt	ggc	ctc	ctc	gaa	ggg	atg	agg	cag	gca	gat	att	cgc	1869
Ser	Ala	Arg	Gly	Gly	Leu	Glu	Gly	Met	Arg	Gln	Ala	Asp	Ile	Arg		
				290				295						300		
tat	gtc	aag	aca	gtc	tat	gac	acc	cgg	agg	gga	gtc	tca	gca	gag	tat	1917
Tyr	Val	Lys	Thr	Val	Tyr	Asp	Thr	Arg	Arg	Gly	Val	Ser	Ala	Glu	Tyr	
					310					315					320	
gag	gtg	aac	tct	tca	gcc	ctg	ctg	ctt	caa	ggt	agg	gag	gcc	cga	gcc	1965
Glu	Val	Asn	Ser	Ser	Ala	Leu	Leu	Leu	Gln	Gly	Arg	Glu	Ala	Arg	Ala	
				325					330					335		
tca	gca	aat	ggt	cag	ggc	tat	gat	aaa	tg	tct	aat	att	cct	cgg	ggc	2013
Ser	Ala	Asn	Gly	Gln	Gly	Tyr	Asp	Lys	Trp	Ser	Asn	Ile	Pro	Arg	Gly	
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aag	gga	gtg	cca	ccc	cca	tcc	tg	agc	cag	cag	tgc	ccc	agt	tcc	ttg	2061
Lys	Gly	Val	Pro	Pro	Pro	Ser	Trp	Ser	Gln	Gln	Cys	Pro	Ser	Ser	Leu	
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gag	act	gcc	acg	gac	aac	ctt	cct	cct	aag	gtg	ggt	gca	ccc	ctg	cct	2109
Glu	Thr	Ala	Thr	Asp	Asn	Leu	Pro	Pro	Lys	Val	Gly	Ala	Pro	Leu	Pro	
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cca	gct	cgg	agt	gac	agt	tac	gca	gca	ttt	cgg	cac	cgt	gag	cgg	ccc	2157
Pro	Ala	Arg	Ser	Asp	Ser	Tyr	Ala	Ala	Phe	Arg	His	Arg	Glu	Arg	Pro	
					390					395					400	
agc	tcc	tg	tct	agc	ctt	gat	cag	aaa	cgg	ctc	tgc	cgg	cct	cag	gca	2205
Ser	Ser	Trp	Ser	Ser	Leu	Asp	Gln	Lys	Arg	Leu	Cys	Arg	Pro	Gln	Ala	
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aac	tct	tta	ggc	tcc	ctg	aag	tct	cca	ttc	ata	gag	gag	cag	ctg	cat	2253

Asn	Ser	Leu	Gly	Ser	Leu	Lys	Ser	Pro	Phe	Ile	Glu	Glu	Gln	Leu	His	
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act	gtg	ctg	gag	aag	agt	cca	gag	aac	agc	ccc	cca	gtg	aag	ccc	aag	2301
Thr	Val	Leu	Glu	Lys	Ser	Pro	Glu	Asn	Ser	Pro	Pro	Val	Lys	Pro	Lys	
			435				440					445				
cat	aac	tat	acc	cag	aag	gcc	caa	cct	ggc	caa	cct	ctg	ctg	ccg	acc	2349
His	Asn	Tyr	Thr	Gln	Lys	Ala	Gln	Pro	Gly	Gln	Pro	Leu	Leu	Pro	Thr	
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agc	atc	tac	gcg	gta	cct	tcc	ctg	gag	cca	cac	ttt	gcc	cag	gtg	cct	2397
Ser	Ile	Tyr	Ala	Val	Pro	Ser	Leu	Glu	Pro	His	Phe	Ala	Gln	Val	Pro	
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cag	cct	tct	gtg	agt	agc	aac	ggg	atg	ctc	tac	cct	gca	ctg	gcc	aag	2445
Gln	Pro	Ser	Val	Ser	Ser	Asn	Gly	Met	Leu	Tyr	Pro	Ala	Leu	Ala	Lys	
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gag	agt	gga	tac	ata	gcc	cct	cag	gga	gca	tgc	aac	aag	atg	gct	acc	2493
Glu	Ser	Gly	Tyr	Ile	Ala	Pro	Gln	Gly	Ala	Cys	Asn	Lys	Met	Ala	Thr	
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Ile	Asp	Glu	Asn	Gly	Asn	Gln	Asn	Gly	Ser	Gly	Arg	Pro	Gly	Phe	Ala	
			515				520					525				
ttc	tgc	cag	ccc	tta	gaa	cat	gac	ttg	ctg	tcc	cca	gtg	gag	aag	aaa	2589
Phe	Cys	Gln	Pro	Leu	Glu	His	Asp	Leu	Leu	Ser	Pro	Val	Glu	Lys	Lys	
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cca	gaa	gct	aca	gcc	aag	tat	gtc	ccc	tcc	aaa	gtc	cat	ttc	tgt	tca	2637
Pro	Glu	Ala	Thr	Ala	Lys	Tyr	Val	Pro	Ser	Lys	Val	His	Phe	Cys	Ser	
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gtg	cct	gaa	aat	gag	gag	gat	gcc	tcc	ctg	aag	aga	cat	ctc	aca	cct	2685
Val	Pro	Glu	Asn	Glu	Glu	Asp	Ala	Ser	Leu	Lys	Arg	His	Leu	Thr	Pro	
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ccc	caa	ggc	aac	agc	cca	cat	tcc	aat	gag	aga	aag	agc	acc	cac	agt	2733
Pro	Gln	Gly	Asn	Ser	Pro	His	Ser	Asn	Glu	Arg	Lys	Ser	Thr	His	Ser	
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aac	aaa	cca	tct	tct	cat	ccc	cac	agc	ctc	aaa	tgc	cct	cag	gct	cag	2781
Asn	Lys	Pro	Ser	Ser	His	Pro	His	Ser	Leu	Lys	Cys	Pro	Gln	Ala	Gln	
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gcc	tgg	caa	gcg	ggg	gaa	gac	aag	aga	tct	tcc	agg	ctc	tca	gag	ccc	2829
Ala	Trp	Gln	Ala	Gly	Glu	Asp	Lys	Arg	Ser	Ser	Arg	Leu	Ser	Glu	Pro	
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Trp	Glu	Gly	Asp	Phe	Gln	Glu	Asp	His	Asn	Ala	Asn	Leu	Trp	Arg	Arg	
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ctg	gag	aga	gaa	ggc	cta	ggc	cag	agc	ctg	tca	ggc	aac	ttt	ggc	aag	2925
Leu	Glu	Arg	Glu	Gly	Leu	Gly	Gln	Ser	Leu	Ser	Gly	Asn	Phe	Gly	Lys	
				645					650					655		
acc	aag	tca	gcc	ttc	tca	tct	ctc	cag	aac	att	cct	gag	agt	ctg	aga	2973
Thr	Lys	Ser	Ala	Phe	Ser	Ser	Leu	Gln	Asn	Ile	Pro	Glu	Ser	Leu	Arg	
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Arg	His	Ser	Ser	Leu	Glu	Leu	Gly	Arg	Gly	Thr	Gln	Glu	Gly	Tyr	Pro	
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Gly	Gly	Arg	Pro	Thr	Cys	Ala	Val	Asn	Thr	Lys	Ala	Glu	Asp	Pro	Gly	
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agg	aaa	gcc	gct	cct	gac	ctc	ggg	agc	cat	ctg	gac	cgg	cag	gtt	tcc	3117
Arg	Lys	Ala	Ala	Pro	Asp	Leu	Gly	Ser	His	Leu	Asp	Arg	Gln	Val	Ser	
705					710					715					720	
tac	ccg	cgg	ccc	gag	ggg	agg	acc	ggt	gcc	tcg	gct	tct	ttc	aac	agc	3165
Tyr	Pro	Arg	Pro	Glu	Gly	Arg	Thr	Gly	Ala	Ser	Ala	Ser	Phe	Asn	Ser	
				725					730					735		
aca	gac	cca	agt	ccc	gaa	gag	ccg	cct	gcc	ccc	tcg	cac	ccg	cac	aca	3213
Thr	Asp	Pro	Ser	Pro	Glu	Glu	Pro	Pro	Ala	Pro	Ser	His	Pro	His	Thr	
			740					745					750			
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Ser	Ser	Leu	Gly	Arg	Arg	Gly	Pro	Gly	Pro	Gly	Ser	Ala	Ser	Ala	Leu	
		755					760					765				
cag	ggc	ttt	cag	tac	ggg	aag	ccc	cac	tgc	tcg	gtg	ctg	gag	aag	gtc	3309
Gln	Gly	Phe	Gln	Tyr	Gly	Lys	Pro	His	Cys	Ser	Val	Leu	Glu	Lys	Val	
	770					775					780					
tcc	aaa	ttc	gag	cag	cga	gag	caa	ggg	agc	cag	aga	ccg	agt	gtg	ggc	3357
Ser	Lys	Phe	Glu	Gln	Arg	Glu	Gln	Gly	Ser	Gln	Arg	Pro	Ser	Val	Gly	
	785				790					795					800	
ggc	tct	ggt	ttt	ggc	cat	aac	tat	agg	ccc	cac	agg	acc	gtc	tca	act	3405
Gly	Ser	Gly	Phe	Gly	His	Asn	Tyr	Arg	Pro	His	Arg	Thr	Val	Ser	Thr	
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tcc	agt	act	tct	ggg	aat	gac	ttc	gag	gag	aca	aaa	gca	cac	att	cgt	3453
Ser	Ser	Thr	Ser	Gly	Asn	Asp	Phe	Glu	Glu	Thr	Lys	Ala	His	Ile	Arg	
			820					825					830			
ttc	tct	gag	tca	gct	gaa	ccc	cta	ggc	aac	ggg	gag	cag	cac	ttc	aaa	3501
Phe	Ser	Glu	Ser	Ala	Glu	Pro	Leu	Gly	Asn	Gly	Glu	Gln	His	Phe	Lys	
		835					840					845				
aac	ggg	gag	ctg	aag	ttg	gaa	gag	gct	tcc	cgg	cag	ccc	tgc	ggt	cag	3549
Asn	Gly	Glu	Leu	Lys	Leu	Glu	Glu	Ala	Ser	Arg	Gln	Pro	Cys	Gly	Gln	
	850					855					860					
cag	ctg	agc	gga	gga	gcg	tcg	gac	agc	ggc	cgt	ggc	ccc	cag	agg	ccg	3597
Gln	Leu	Ser	Gly	Gly	Ala	Ser	Asp	Ser	Gly	Arg	Gly	Pro	Gln	Arg	Pro	
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gac	gct	cgg	ctc	ctc	cgt	agc	cag	agc	acc	ttc	cag	ctc	tcc	agc	gag	3645
Asp	Ala	Arg	Leu	Leu	Arg	Ser	Gln	Ser	Thr	Phe	Gln	Leu	Ser	Ser	Glu	
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Pro	Glu	Arg	Glu	Pro	Glu	Trp	Arg	Asp	Arg	Pro	Gly	Ser	Pro	Glu	Ser	
			900					905					910			
ccc	ctg	ctg	gat	gcc	ccc	ttc	agc	cgc	gcc	tac	cgg	aac	agc	atc	aag	3741
Pro	Leu	Leu	Asp	Ala	Pro	Phe	Ser	Arg	Ala	Tyr	Arg	Asn	Ser	Ile	Lys	
		915					920					925				
gac	gca	cag	tcc	cgt	gtc	ttg	ggg	gcc	acc	tcc	ttt	cga	cgt	cga	gac	3789
Asp	Ala	Gln	Ser	Arg	Val	Leu	Gly	Ala	Thr	Ser	Phe	Arg	Arg	Arg	Asp	
	930					935					940					
ctg	gag	ctg	ggg	gcg	ccc	gtg	gcg	tcg	agg	tcc	tgg	cgg	cca	cgg	cct	3837
Leu	Glu	Leu	Gly	Ala	Pro	Val	Ala	Ser	Arg	Ser	Trp	Arg	Pro	Arg	Pro	
	945				950				955						960	
tcc	tcg	gcc	cac	gtg	ggg	ctg	cgg	agc	ccc	gag	gcg	tcg	gcc	tcc	gcc	3885



Ser Ser Ala His Val Gly Leu Arg Ser Pro Glu Ala Ser Ala Ser Ala	965	970	975	
tcc ccg cac acg ccc cgg gag cgg cac agc gtg acc cct gct gag ggc				3933
Ser Pro His Thr Pro Arg Glu Arg His Ser Val Thr Pro Ala Glu Gly	980	985	990	
gac ctg gcc agg ccc gtg ccc cct gcc gcc cgg aga ggt gct cgc cgg				3981
Asp Leu Ala Arg Pro Val Pro Pro Ala Ala Arg Arg Gly Ala Arg Arg	995	1000	1005	
cgc ctg act ccc gag cag aag aag cgc tcc tac tcg gag ccc gag				4026
Arg Leu Thr Pro Glu Gln Lys Lys Arg Ser Tyr Ser Glu Pro Glu	1010	1015	1020	
aag atg aac gag gtg ggg atc gtg gag gag gcc gaa ccg gca ccc				4071
Lys Met Asn Glu Val Gly Ile Val Glu Glu Ala Glu Pro Ala Pro	1025	1030	1035	
ctg ggc ccg cag aga aat ggg atg cgt ttc ccg gag agc agc gtg				4116
Leu Gly Pro Gln Arg Asn Gly Met Arg Phe Pro Glu Ser Ser Val	1040	1045	1050	
gcc gac cgg cgc cgt ctc ttc gag cgc gat gcc aag gcc tgc tcc				4161
Ala Asp Arg Arg Arg Leu Phe Glu Arg Asp Gly Lys Ala Cys Ser	1055	1060	1065	
acg ctc agc ctg tcg ggg ccc gag ctg aag cag ttc cag cag agc				4206
Thr Leu Ser Leu Ser Gly Pro Glu Leu Lys Gln Phe Gln Gln Ser	1070	1075	1080	
gcc ctg gcg gac tac atc cag cgc aag acc gcc aag ccg cct acc				4251
Ala Leu Ala Asp Tyr Ile Gln Arg Lys Thr Gly Lys Arg Pro Thr	1085	1090	1095	
tcc gcc gcc ggc tgc agc ctc cag gag ccc ggg cca ctg cgt gag				4296
Ser Ala Ala Gly Cys Ser Leu Gln Glu Pro Gly Pro Leu Arg Glu	1100	1105	1110	
cgc gcc cag agt gcc tac ctc cag ccc ggc ccc gcg gcg ctc gaa				4341
Arg Ala Gln Ser Ala Tyr Leu Gln Pro Gly Pro Ala Ala Leu Glu	1115	1120	1125	
ggc tcc gcc ctc gcc tcg gcc tcc agc ttg agc tca ctg cgg gag				4386
Gly Ser Gly Leu Ala Ser Ala Ser Ser Leu Ser Ser Leu Arg Glu	1130	1135	1140	
ccc agc ctg cag ccc cgc agg gag gcc acg ctc ctg ccg gcc aca				4431
Pro Ser Leu Gln Pro Arg Arg Glu Ala Thr Leu Leu Pro Ala Thr	1145	1150	1155	
gtt gca gaa acc cag cag gct ccc cga gat cgc agc agc tcc ttc				4476
Val Ala Glu Thr Gln Gln Ala Pro Arg Asp Arg Ser Ser Ser Phe	1160	1165	1170	
gcc ggt gcc cgc cgc ctc ggg gaa cgg cga cgc ggg gac ctg ctt				4521
Ala Gly Gly Arg Arg Leu Gln Glu Arg Arg Arg Gly Asp Leu Leu	1175	1180	1185	
agc gga gca aac ggt gga aca agg ggc acc cag aga ggg gat gag				4566
Ser Gly Ala Asn Gly Gly Thr Arg Gly Thr Gln Arg Gly Asp Glu	1190	1195	1200	
acc ccc agg gag cca tcc tcc tgg ggg gcc agg gcc ggg aag tcc				4611
Thr Pro Arg Glu Pro Ser Ser Trp Gly Ala Arg Ala Gly Lys Ser	1205	1210	1215	
atg tcg gcc gag gac ctg ctg gaa cgc tcg gac gtc ctt gcg ggc				4656

Met	Ser	Ala	Glu	Asp	Leu	Leu	Glu	Arg	Ser	Asp	Val	Leu	Ala	Gly		
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cct	gtc	cat	gtg	agg	tcc	agg	tca	tct	ccc	gcc	acc	gca	gac	aag	4701	
Pro	Val	His	Val	Arg	Ser	Arg	Ser	Ser	Pro	Ala	Thr	Ala	Asp	Lys		
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cgc	cag	gat	gtg	ctt	ttg	ggg	caa	gac	agt	ggc	ttt	ggt	ctt	gtg	4746	
Arg	Gln	Asp	Val	Leu	Leu	Gly	Gln	Asp	Ser	Gly	Phe	Gly	Leu	Val		
1250						1255					1260					
aag	gat	cca	tgt	tat	ttg	gct	ggg	cct	gga	tct	agg	tca	ctc	agt	4791	
Lys	Asp	Pro	Cys	Tyr	Leu	Ala	Gly	Pro	Gly	Ser	Arg	Ser	Leu	Ser		
1265						1270					1275					
tgt	tca	gaa	aga	ggc	caa	gaa	gag	atg	ctg	ctg	ctc	ttc	cac	cat	4836	
Cys	Ser	Glu	Arg	Gly	Gln	Glu	Glu	Met	Leu	Leu	Leu	Phe	His	His		
1280						1285					1290					
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Leu	Thr	Pro	Arg	Trp	Gly	Gly	Ser	Gly	Cys	Lys	Ala	Ile	Gly	Asp		
1295						1300					1305					
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Ser	Ser	Val	Pro	Ser	Glu	Cys	Pro	Gly	Thr	Leu	Asp	His	Gln	Arg		
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caa	gcc	agt	agg	aca	ccc	tgc	ccc	agg	cca	cca	ctg	gca	gga	acg	4971	
Gln	Ala	Ser	Arg	Thr	Pro	Cys	Pro	Arg	Pro	Pro	Leu	Ala	Gly	Thr		
1325						1330					1335					
caa	ggg	ctg	gtc	aca	gac	acc	agg	gct	gca	ccc	ctg	acc	cca	att	5016	
Gln	Gly	Leu	Val	Thr	Asp	Thr	Arg	Ala	Ala	Pro	Leu	Thr	Pro	Ile		
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ggc	acc	cct	ctg	cct	tca	gcc	att	ccc	tct	ggc	tac	tgc	tca	cag	5061	
Gly	Thr	Pro	Leu	Pro	Ser	Ala	Ile	Pro	Ser	Gly	Tyr	Cys	Ser	Gln		
1355						1360					1365					
gac	ggg	cag	aca	ggg	cga	cag	cct	ctc	ccg	ccc	tac	acc	cct	gcc	5106	
Asp	Gly	Gln	Thr	Gly	Arg	Gln	Pro	Leu	Pro	Pro	Tyr	Thr	Pro	Ala		
1370						1375					1380					
atg	atg	cac	aga	agc	aat	ggg	cac	acc	ctg	acc	cag	cct	ccc	ggg	5151	
Met	Met	His	Arg	Ser	Asn	Gly	His	Thr	Leu	Thr	Gln	Pro	Pro	Gly		
1385						1390					1395					
cca	aga	ggc	tgt	gag	ggc	gat	ggc	cca	gag	cat	ggg	gta	gaa	gag	5196	
Pro	Arg	Gly	Cys	Glu	Gly	Asp	Gly	Pro	Glu	His	Gly	Val	Glu	Glu		
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gga	acg	agg	aag	agg	gtc	tgc	ctg	cct	cag	tgg	cca	cct	cct	tct	5241	
Gly	Thr	Arg	Lys	Arg	Val	Ser	Leu	Pro	Gln	Trp	Pro	Pro	Pro	Ser		
1415						1420					1425					
cga	gca	aag	tgg	gcc	cac	gca	gcc	aga	gag	gac	agc	ctt	cct	gag	5286	
Arg	Ala	Lys	Trp	Ala	His	Ala	Ala	Arg	Glu	Asp	Ser	Leu	Pro	Glu		
1430						1435					1440					
gaa	tcc	tca	gcc	cct	gat	ttt	gca	aac	ctg	aag	cac	tat	caa	aaa	5331	
Glu	Ser	Ser	Ala	Pro	Asp	Phe	Ala	Asn	Leu	Lys	His	Tyr	Gln	Lys		
1445						1450					1455					
cag	cag	agt	ctt	cca	agt	tta	tgc	agc	act	tct	gac	cca	gac	aca	5376	
Gln	Gln	Ser	Leu	Pro	Ser	Leu	Cys	Ser	Thr	Ser	Asp	Pro	Asp	Thr		
1460						1465					1470					
cct	ctt	ggg	gcc	ccg	agc	act	cca	ggg	agg	atc	tcc	ctc	cga	ata	5421	

Pro Leu Gly Ala Pro Ser Thr	Pro Gly Arg Ile Ser	Leu Arg Ile	
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tct gag tct gtc ctg cgg gac	tcc ccg cca cct cat	gag gat tat	5466
Ser Glu Ser Val Leu Arg Asp	Ser Pro Pro Pro His	Glu Asp Tyr	
1490	1495	1500	
gaa gac gaa gtg ttt gtg agg	gat ccg cac ccc aag	gcc acg tcc	5511
Glu Asp Glu Val Phe Val Arg	Asp Pro His Pro Lys	Ala Thr Ser	
1505	1510	1515	
agc ccc aca ttt gaa cct ctt	ccc cca ccc cca cct	cct cca ccg	5556
Ser Pro Thr Phe Glu Pro Leu	Pro Pro Pro Pro Pro	Pro Pro Pro	
1520	1525	1530	
agt cag gaa acc ccg gtg tat	agc atg gat gac ttc	cct cca cct	5601
Ser Gln Glu Thr Pro Val Tyr	Ser Met Asp Asp Phe	Pro Pro Pro	
1535	1540	1545	
cct ccc cac act gta tgt gag	gcg cag ctg gac agt	gag gat ccc	5646
Pro Pro His Thr Val Cys Glu	Ala Gln Leu Asp Ser	Glu Asp Pro	
1550	1555	1560	
gag ggg cca cgc ccc agc ttc	aac aaa ctt tct aaa	gtg aca att	5691
Glu Gly Pro Arg Pro Ser Phe	Asn Lys Leu Ser Lys	Val Thr Ile	
1565	1570	1575	
gca agg gaa agg cac atg cct	ggt gca gcc cat gtg	gta ggt agt	5736
Ala Arg Glu Arg His Met Pro	Gly Ala Ala His Val	Val Gly Ser	
1580	1585	1590	
cag aca ctg gct tcc aga ctc	caa act tct atc aag	ggt tca gag	5781
Gln Thr Leu Ala Ser Arg Leu	Gln Thr Ser Ile Lys	Gly Ser Glu	
1595	1600	1605	
gct gag tcc aca cca ccc tcc	ttc atg agc gtt cac	gcc caa ctt	5826
Ala Glu Ser Thr Pro Pro Ser	Phe Met Ser Val His	Ala Gln Leu	
1610	1615	1620	
gct ggg tct ctt ggt ggg cag	cca gca ccc atc cag	act caa agc	5871
Ala Gly Ser Leu Gly Gly Gln	Pro Ala Pro Ile Gln	Thr Gln Ser	
1625	1630	1635	
ctc agc cat gat cca gtc agt	gga act cag ggt tta	gaa aag aaa	5916
Leu Ser His Asp Pro Val Ser	Gly Thr Gln Gly Leu	Glu Lys Lys	
1640	1645	1650	
gtc agt cct gat cct cag aag	agt tca gaa gac atc	aga aca gag	5961
Val Ser Pro Asp Pro Gln Lys	Ser Ser Glu Asp Ile	Arg Thr Glu	
1655	1660	1665	
gct ttg gcc aag gaa att gtc	cac caa gac aaa tct	cta gca gac	6006
Ala Leu Ala Lys Glu Ile Val	His Gln Asp Lys Ser	Leu Ala Asp	
1670	1675	1680	
att ttg gat cca gac tcc agg	ctg aag aca aca atg	gac ctg atg	6051
Ile Leu Asp Pro Asp Ser Arg	Leu Lys Thr Thr Met	Asp Leu Met	
1685	1690	1695	
gaa ggt ttg ttt ccc cga gat	gtg aac ttg ctg aag	gaa aac agt	6096
Glu Gly Leu Phe Pro Arg Asp	Val Asn Leu Leu Lys	Glu Asn Ser	
1700	1705	1710	
gta aag agg aag gcc ata cag	aga act gtc agc tct	tca gga tgt	6141
Val Lys Arg Lys Ala Ile Gln	Arg Thr Val Ser Ser	Ser Gly Cys	
1715	1720	1725	
gaa ggc aag agg aat gaa gac	aag gaa gca gtg agc	atg ttg gtt	6186

Glu Gly Lys Arg Asn Glu Asp Lys Glu Ala Val Ser Met Leu Val	
1730 1735 1740	
aac tgc cct gcc tac tac agt gtg tct gct ccc aag gct gag cta	6231
Asn Cys Pro Ala Tyr Tyr Ser Val Ser Ala Pro Lys Ala Glu Leu	
1745 1750 1755	
ctg aac aaa atc aaa gag atg cca gca gaa gtg aat gag gaa gag	6276
Leu Asn Lys Ile Lys Glu Met Pro Ala Glu Val Asn Glu Glu Glu	
1760 1765 1770	
gaa cag gca gat gtc aat gaa aag aag gct gag ctc att gga agt	6321
Glu Gln Ala Asp Val Asn Glu Lys Lys Ala Glu Leu Ile Gly Ser	
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Leu Thr His Lys Leu Glu Thr Leu Gln Glu Ala Lys Gly Ser Leu	
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Leu Thr Asp Ile Lys Leu Asn Asn Ala Leu Gly Glu Glu Val Glu	
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gct ctg atc agc gag ctc tgc aag ccc aat gag ttt gac aag tat	6456
Ala Leu Ile Ser Glu Leu Cys Lys Pro Asn Glu Phe Asp Lys Tyr	
1820 1825 1830	
agg atg ttc ata ggg gat ttg gac aag gtg gtc aac ctg ctg ctc	6501
Arg Met Phe Ile Gly Asp Leu Asp Lys Val Val Asn Leu Leu Leu	
1835 1840 1845	
tcc ctc tcg ggg cgt cta gcc cgt gtt gag aat gtc ctt agc ggc	6546
Ser Leu Ser Gly Arg Leu Ala Arg Val Glu Asn Val Leu Ser Gly	
1850 1855 1860	
ctt ggt gaa gat gcc agt aat gaa gaa agg agc tct ctt tac gag	6591
Leu Gly Glu Asp Ala Ser Asn Glu Glu Arg Ser Ser Leu Tyr Glu	
1865 1870 1875	
aaa agg aag atc ctg gct ggt cag cat gag gat gcc cgg gag ctg	6636
Lys Arg Lys Ile Leu Ala Gly Gln His Glu Asp Ala Arg Glu Leu	
1880 1885 1890	
aag gag aac ctg gat cgc agg gag cga gta gtg ctg ggc atc ttg	6681
Lys Glu Asn Leu Asp Arg Arg Glu Arg Val Val Leu Gly Ile Leu	
1895 1900 1905	
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Ala Asn Tyr Leu Ser Glu Glu Gln Leu Gln Asp Tyr Gln His Phe	
1910 1915 1920	
gtg aaa atg aag tcc acg ctc ctc att gag caa cgg aag ctg gat	6771
Val Lys Met Lys Ser Thr Leu Leu Ile Glu Gln Arg Lys Leu Asp	
1925 1930 1935	
gac aag atc aag ctg ggc cag gag cag gtc aag tgt ctg ctg gag	6816
Asp Lys Ile Lys Leu Gly Gln Glu Gln Val Lys Cys Leu Leu Glu	
1940 1945 1950	
agc ctg ccc tca gat ttc att ccc aag gct ggg gcc ctg gct ctg	6861
Ser Leu Pro Ser Asp Phe Ile Pro Lys Ala Gly Ala Leu Ala Leu	
1955 1960 1965	
ccc cca aac ctc acg agt gag ccc att cct gct ggg ggc tgt act	6906
Pro Pro Asn Leu Thr Ser Glu Pro Ile Pro Ala Gly Gly Cys Thr	
1970 1975 1980	
ttc agt ggt att ttc cca aca tta acc tct cca ctt taacctcttc	6952

Phe Ser Gly Ile Phe Pro Thr Leu Thr Ser Pro Leu  
 1985 1990 1995

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cagtacaaac cactgtttga actatctggg ttattggtgt ttgttcctga tgaaaggaaa 7072

aaaattctct ccaggaggaa gcctttttcc ttcttgccct tcttgattga tcttctgaga 7132

gctcgaatgc tgctggacac gtaccccttt ctattattac ttgttagtag aaagaaagtt 7192

aatgaaactg agaactgatt ggagggtggt tgatcattta gtttttaaca ggctgaggca 7252

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aaatggaaaa gatcactatg ttgtgtgtgc taaccactta ttgattctg tttgtggtg 7492

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<211> 1995

<212> PRT

<213> NM\_020859 ShrmL, Shroom-related protein

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 35 40 45

Glu Pro Leu Ile Ile Ser Lys Val Glu Glu Gly Gly Lys Ala Asp Thr  
 50 55 60

Leu Ser Ser Lys Leu Gln Ala Gly Asp Glu Val Val His Ile Asn Glu  
 65 70 75 80

Val Thr Leu Ser Ser Ser Arg Lys Glu Ala Val Ser Leu Val Lys Gly  
 85 90 95

Ser Tyr Lys Thr Leu Arg Leu Val Val Arg Arg Asp Val Cys Thr Asp  
 100 105 110

Pro Gly His Ala Asp Thr Gly Ala Ser Asn Phe Val Ser Pro Glu His  
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Leu Thr Ser Gly Pro Gln His Arg Lys Ala Ala Trp Ser Gly Gly Val  
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Lys Leu Arg Leu Lys His Arg Ser Ser Glu Pro Ala Gly Arg Pro His  
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Ser Trp His Thr Thr Lys Ser Gly Glu Lys Gln Pro Asp Ala Ser Met  
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Met Gln Ile Ser Gln Gly Met Ile Gly Pro Pro Trp His Gln Ser Tyr  
180 185 190

His Ser Ser Ser Ser Thr Ser Asp Leu Ser Asn Tyr Asp His Ala Tyr  
195 200 205

Leu Arg Arg Ser Pro Asp Gln Cys Ser Ser Gln Gly Ser Met Glu Ser  
210 215 220

Leu Glu Pro Ser Gly Ala Tyr Pro Pro Cys His Leu Ser Pro Ala Lys  
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Ser Thr Gly Ser Ile Asp Gln Leu Ser His Phe His Asn Lys Arg Asp  
245 250 255

Ser Ala Tyr Ser Ser Phe Ser Thr Ser Ser Ser Ile Leu Glu Tyr Pro  
260 265 270

His Pro Gly Ile Ser Ala Arg Glu Arg Ser Gly Ser Met Asp Asn Thr  
275 280 285

Ser Ala Arg Gly Gly Leu Leu Glu Gly Met Arg Gln Ala Asp Ile Arg  
290 295 300

Tyr Val Lys Thr Val Tyr Asp Thr Arg Arg Gly Val Ser Ala Glu Tyr  
305 310 315 320

Glu Val Asn Ser Ser Ala Leu Leu Leu Gln Gly Arg Glu Ala Arg Ala  
325 330 335

Ser Ala Asn Gly Gln Gly Tyr Asp Lys Trp Ser Asn Ile Pro Arg Gly  
340 345 350

Lys Gly Val Pro Pro Pro Ser Trp Ser Gln Gln Cys Pro Ser Ser Leu  
355 360 365

Glu Thr Ala Thr Asp Asn Leu Pro Pro Lys Val Gly Ala Pro Leu Pro  
370 375 380

Pro Ala Arg Ser Asp Ser Tyr Ala Ala Phe Arg His Arg Glu Arg Pro  
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Ser Ser Trp Ser Ser Leu Asp Gln Lys Arg Leu Cys Arg Pro Gln Ala  
405 410 415

Asn Ser Leu Gly Ser Leu Lys Ser Pro Phe Ile Glu Glu Gln Leu His  
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Thr Val Leu Glu Lys Ser Pro Glu Asn Ser Pro Pro Val Lys Pro Lys  
435 440 445

His Asn Tyr Thr Gln Lys Ala Gln Pro Gly Gln Pro Leu Leu Pro Thr  
450 455 460

Ser Ile Tyr Ala Val Pro Ser Leu Glu Pro His Phe Ala Gln Val Pro  
465 470 475 480

Gln Pro Ser Val Ser Ser Asn Gly Met Leu Tyr Pro Ala Leu Ala Lys  
485 490 495

Glu Ser Gly Tyr Ile Ala Pro Gln Gly Ala Cys Asn Lys Met Ala Thr  
500 505 510

Ile Asp Glu Asn Gly Asn Gln Asn Gly Ser Gly Arg Pro Gly Phe Ala  
515 520 525

Phe Cys Gln Pro Leu Glu His Asp Leu Leu Ser Pro Val Glu Lys Lys  
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Pro Glu Ala Thr Ala Lys Tyr Val Pro Ser Lys Val His Phe Cys Ser  
545 550 555 560

Val Pro Glu Asn Glu Glu Asp Ala Ser Leu Lys Arg His Leu Thr Pro  
565 570 575

Pro Gln Gly Asn Ser Pro His Ser Asn Glu Arg Lys Ser Thr His Ser  
580 585 590

Asn Lys Pro Ser Ser His Pro His Ser Leu Lys Cys Pro Gln Ala Gln  
595 600 605

Ala Trp Gln Ala Gly Glu Asp Lys Arg Ser Ser Arg Leu Ser Glu Pro  
610 615 620

Trp Glu Gly Asp Phe Gln Glu Asp His Asn Ala Asn Leu Trp Arg Arg  
625 630 635 640

Leu Glu Arg Glu Gly Leu Gly Gln Ser Leu Ser Gly Asn Phe Gly Lys  
645 650 655

Thr Lys Ser Ala Phe Ser Ser Leu Gln Asn Ile Pro Glu Ser Leu Arg  
660 665 670

Arg His Ser Ser Leu Glu Leu Gly Arg Gly Thr Gln Glu Gly Tyr Pro  
675 680 685

Gly Gly Arg Pro Thr Cys Ala Val Asn Thr Lys Ala Glu Asp Pro Gly  
690 695 700

Arg Lys Ala Ala Pro Asp Leu Gly Ser His Leu Asp Arg Gln Val Ser  
705 710 715 720

Tyr Pro Arg Pro Glu Gly Arg Thr Gly Ala Ser Ala Ser Phe Asn Ser  
725 730 735

Thr Asp Pro Ser Pro Glu Glu Pro Pro Ala Pro Ser His Pro His Thr  
740 745 750

Ser Ser Leu Gly Arg Arg Gly Pro Gly Pro Gly Ser Ala Ser Ala Leu  
755 760 765

Gln Gly Phe Gln Tyr Gly Lys Pro His Cys Ser Val Leu Glu Lys Val  
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Ser Lys Phe Glu Gln Arg Glu Gln Gly Ser Gln Arg Pro Ser Val Gly  
785 790 795 800

Gly Ser Gly Phe Gly His Asn Tyr Arg Pro His Arg Thr Val Ser Thr  
805 810 815

Ser Ser Thr Ser Gly Asn Asp Phe Glu Glu Thr Lys Ala His Ile Arg  
820 825 830

Phe Ser Glu Ser Ala Glu Pro Leu Gly Asn Gly Glu Gln His Phe Lys  
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Asn Gly Glu Leu Lys Leu Glu Glu Ala Ser Arg Gln Pro Cys Gly Gln  
850 855 860

Gln Leu Ser Gly Gly Ala Ser Asp Ser Gly Arg Gly Pro Gln Arg Pro  
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Asp Ala Arg Leu Leu Arg Ser Gln Ser Thr Phe Gln Leu Ser Ser Glu  
885 890 895

Pro Glu Arg Glu Pro Glu Trp Arg Asp Arg Pro Gly Ser Pro Glu Ser  
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Pro Leu Leu Asp Ala Pro Phe Ser Arg Ala Tyr Arg Asn Ser Ile Lys  
915 920 925

Asp Ala Gln Ser Arg Val Leu Gly Ala Thr Ser Phe Arg Arg Arg Asp  
930 935 940



Leu Glu Leu Gly Ala Pro Val Ala Ser Arg Ser Trp Arg Pro Arg Pro  
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Ser Pro His Thr Pro Arg Glu Arg His Ser Val Thr Pro Ala Glu Gly  
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Asp Leu Ala Arg Pro Val Pro Pro Ala Ala Arg Arg Gly Ala Arg Arg  
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Arg Leu Thr Pro Glu Gln Lys Lys Arg Ser Tyr Ser Glu Pro Glu  
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Leu Gly Pro Gln Arg Asn Gly Met Arg Phe Pro Glu Ser Ser Val  
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Thr Leu Ser Leu Ser Gly Pro Glu Leu Lys Gln Phe Gln Gln Ser  
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Pro Ser Leu Gln Pro Arg Arg Glu Ala Thr Leu Leu Pro Ala Thr  
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Val Ala Glu Thr Gln Gln Ala Pro Arg Asp Arg Ser Ser Ser Phe  
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Ala Gly Gly Arg Arg Leu Gly Glu Arg Arg Arg Gly Asp Leu Leu  
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Ser Gly Ala Asn Gly Gly Thr Arg Gly Thr Gln Arg Gly Asp Glu  
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Thr Pro Arg Glu Pro Ser Ser Trp Gly Ala Arg Ala Gly Lys Ser  
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 Pro Val His Val Arg Ser Arg Ser Ser Pro Ala Thr Ala Asp Lys  
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 Lys Asp Pro Cys Tyr Leu Ala Gly Pro Gly Ser Arg Ser Leu Ser  
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 Cys Ser Glu Arg Gly Gln Glu Glu Met Leu Leu Leu Phe His His  
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 1775 1780 1785  
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 Leu Gly Glu Asp Ala Ser Asn Glu Glu Arg Ser Ser Leu Tyr Glu  
 1865 1870 1875  
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 Lys Glu Asn Leu Asp Arg Arg Glu Arg Val Val Leu Gly Ile Leu  
 1895 1900 1905  
 Ala Asn Tyr Leu Ser Glu Glu Gln Leu Gln Asp Tyr Gln His Phe  
 1910 1915 1920  
 Val Lys Met Lys Ser Thr Leu Leu Ile Glu Gln Arg Lys Leu Asp  
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Met Ala Ala Thr Cys Glu Ile Ser Asn Ile	
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Phe Ser Asn Tyr Phe Ser Ala Met Tyr Ser Ser Glu Asp Ser Thr Leu	
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Ala Ser Val Pro Pro Ala Ala Thr Phe Gly Ala Asp Asp Leu Val Leu	
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Thr Leu Ser Asn Pro Gln Met Ser Leu Glu Gly Thr Glu Lys Ala Ser	
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Trp Ile Ser Tyr Gln Val Glu Lys Asn Lys Tyr Asp Ala Ser Ala Ile	
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Asp Phe Ser Arg Cys Asp Met Asp Gly Ala Thr Leu Cys Asn Cys Ala	
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Leu Glu Glu Leu Arg Leu Val Phe Gly Pro Leu Gly Asp Gln Leu His	
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ctg gat ccc act gat ggc aag ctc ttc ccc agc gat ggt ttt cgt gac Leu Asp Pro Thr Asp Gly Lys Leu Phe Pro Ser Asp Gly Phe Arg Asp 220 225 230	904
tgc aag aag ggg gat ccc aag cac ggg aag cgg aaa cga ggc cgg ccc Cys Lys Lys Gly Asp Pro Lys His Gly Lys Arg Lys Arg Gly Arg Pro 235 240 245 250	952
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Met Ser Leu Glu Gly Thr Glu Lys Ala Ser Trp Leu Gly Glu Gln Pro  
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Gln Phe Trp Ser Lys Thr Gln Val Leu Asp Trp Ile Ser Tyr Gln Val  
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Glu Lys Asn Lys Tyr Asp Ala Ser Ala Ile Asp Phe Ser Arg Cys Asp  
85 90 95

Met Asp Gly Ala Thr Leu Cys Asn Cys Ala Leu Glu Glu Leu Arg Leu  
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Val Phe Gly Pro Leu Gly Asp Gln Leu His Ala Gln Leu Arg Asp Leu  
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Thr Ser Ser Ser Ser Asp Glu Leu Ser Trp Ile Ile Glu Leu Leu Glu  
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Lys Asp Gly Met Ala Phe Gln Glu Ala Leu Asp Pro Gly Pro Phe Asp  
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Gln Gly Ser Pro Phe Ala Gln Glu Leu Leu Asp Asp Gly Gln Gln Ala  
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Ser Pro Tyr His Pro Gly Ser Cys Gly Ala Gly Ala Pro Ser Pro Gly  
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Ser Ser Asp Val Ser Thr Ala Gly Thr Gly Ala Ser Arg Ser Ser His  
195 200 205

Ser Ser Asp Ser Gly Gly Ser Asp Val Asp Leu Asp Pro Thr Asp Gly  
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Lys Leu Phe Pro Ser Asp Gly Phe Arg Asp Cys Lys Lys Gly Asp Pro  
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Lys His Gly Lys Arg Lys Arg Gly Arg Pro Arg Lys Leu Ser Lys Glu  
245 250 255

Tyr Trp Asp Cys Leu Glu Gly Lys Lys Ser Lys His Ala Pro Arg Gly  
260 265 270

Thr His Leu Trp Glu Phe Ile Arg Asp Ile Leu Ile His Pro Glu Leu  
275 280 285

Asn Glu Gly Leu Met Lys Trp Glu Asn Arg His Glu Gly Val Phe Lys  
290 295 300

Phe Leu Arg Ser Glu Ala Val Ala Gln Leu Trp Gly Gln Lys Lys Lys  
305 310 315 320

Asn Ser Asn Met Thr Tyr Glu Lys Leu Ser Arg Ala Met Arg Tyr Tyr  
325 330 335

Tyr Lys Arg Glu Ile Leu Glu Arg Val Asp Gly Arg Arg Leu Val Tyr



340

345

350

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Ser Arg Asn  
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&lt;211&gt; 4020

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&lt;213&gt; NM\_019027 FLJ20273

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 Glu Asn Gly Gln Arg Lys Tyr Gly Gly Pro Pro Pro Gly Trp Glu Gly  
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 Pro His Pro Gln Arg Gly Cys Glu Val Phe Val Gly Lys Ile Pro Arg  
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 Thr Tyr Glu Leu Arg Leu Met Met Phe Asp Gly Lys Asn Arg Gly  
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cag atc gcc gtg gac tgg gcc gag cct gag atc gac gtg gac gag gac Gln Ile Ala Val Asp Trp Ala Glu Pro Glu Ile Asp Val Asp Glu Asp 225 230 235 240	959
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Ser Met Phe Pro Ala Ala Pro Ala Pro Lys Met Ile Glu Asp Gly Lys	
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Ile His Thr Val Glu His Met Ile Ser Pro Ile Ala Val Gln Pro Asp	
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325

330

335

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Thr Leu Ala Tyr Tyr Gly Tyr Pro Tyr Asn Ala Leu Ile Gly Pro Asn  
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Arg Asp Tyr Phe Val Lys Val Ala Ile Pro Ala Ile Gly Ala Gln Tyr  
370 375 380

Ser Met Phe Pro Ala Ala Pro Ala Pro Lys Met Ile Glu Asp Gly Lys  
385 390 395 400

Ile His Thr Val Glu His Met Ile Ser Pro Ile Ala Val Gln Pro Asp  
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Pro Ala Ser Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala  
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Ala Val Ile Pro Thr Val Ser Thr Pro Pro Pro Phe Gln Gly Arg Pro  
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Ile Thr Pro Val Tyr Thr Val Ala Pro Asn Val Gln Arg Ile Pro Thr  
450 455 460

Ala Gly Ile Tyr Gly Ala Ser Tyr Val Pro Phe Ala Ala Pro Ala Thr  
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Ala Thr Ile Ala Thr Leu Gln Lys Asn Ala Ala Ala Ala Ala Ala Val  
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				Met	Pro	His	Asn	Ser								
				1				5								
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Ile	Arg	Ser	Gly	His	Gly	Gly	Leu	Asn	Gln	Leu	Gly	Gly	Ala	Phe	Val	
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Thr	Lys	Val	Gln	Gln	Pro	Phe	Asn	Leu	Pro	Met	Asp	Ser	Cys	Val	Ala	
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acc	aag	tcc	ctg	agt	ccc	gga	cac	acg	ctg	atc	ccc	agc	tca	gct	gta	655
Thr	Lys	Ser	Leu	Ser	Pro	Gly	His	Thr	Leu	Ile	Pro	Ser	Ser	Ala	Val	
150					155				160					165		
act	ccc	ccg	gag	tca	ccc	cag	tcg	gat	tcc	ctg	ggc	tcc	acc	tac	tcc	703
Thr	Pro	Pro	Glu	Ser	Pro	Gln	Ser	Asp	Ser	Leu	Gly	Ser	Thr	Tyr	Ser	
			170					175						180		
atc	aat	ggg	ctc	ctg	ggc	atc	gct	cag	cct	ggc	agc	gac	aag	agg	aaa	751
Ile	Asn	Gly	Leu	Leu	Gly	Ile	Ala	Gln	Pro	Gly	Ser	Asp	Lys	Arg	Lys	
			185					190								

120

cag cac cac ctc gag ccg ctc gag tgc cca ttt gag cgg cag cac tac 895  
 Gln His His Leu Glu Pro Leu Glu Cys Pro Phe Glu Arg Gln His Tyr  
 230 235 240 245  
 cca gag gcc tat gcc tcc ccc agc cac acc aaa ggc gag cag ggc ctc 943  
 Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys Gly Glu Gln Gly Leu  
 250 255 260  
 tac ccg ctg ccc ttg ctc aac agc acc ctg gac gac ggg aag gcc acc 991  
 Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp Asp Gly Lys Ala Thr  
 265 270 275  
 ctg acc cct tcc aac acg cca ctg ggg cgc aac ctc tcg act cac cag 1039  
 Leu Thr Pro Ser Asn Thr Pro Leu Gly Arg Asn Leu Ser Thr His Gln  
 280 285 290  
 acc tac ccc gtg gtg gca gct ccg ccc ttt tgg atc tgc agc aag tcg 1087  
 Thr Tyr Pro Val Val Ala Gct Ala Pro Pro Phe Trp Ile Cys Ser Lys Ser  
 295 300 305  
 gct ccg ggg tcc cgc cct tca atg cct ttc ccc atg ctg cct ccg tgt 1135  
 Ala Pro Gly Ser Arg Pro Ser Met Pro Phe Pro Met Leu Pro Pro Cys  
 310 315 320 325  
 acg ggc agt tca cgg gcc agg ccc tcc tct cag ggc gag aga tgg tgg 1183  
 Thr Gly Ser Ser Arg Ala Arg Pro Ser Ser Gln Gly Glu Arg Trp Trp  
 330 335 340  
 ggc cca cgc tgc ccg gat acc cac ccc aca tcc cca cca gcg gac agg 1231  
 Gly Pro Arg Cys Pro Asp Thr His Pro Thr Ser Pro Pro Ala Asp Arg  
 345 350 355  
 gca gct atg cct cct ctg cca tcg cag gca tgg tgg cag gaa gtg aat 1279  
 Ala Ala Met Pro Pro Leu Pro Ser Gln Ala Trp Trp Gln Glu Val Asn  
 360 365 370  
 act ctg gca atg cct atg gcc aca ccc cct act cct cct aca gcg agg 1327  
 Thr Leu Ala Met Pro Met Ala Thr Pro Pro Thr Pro Pro Thr Ala Arg  
 375 380 385  
 cct ggg gct tcc cca act cca gct tgc tgagttcccc atattattac 1374  
 Pro Gly Ala Ser Pro Thr Pro Ala Cys  
 390 395  
 agttccacat caaggccgag tgcaccgccc accactgcc aaggcctttga ccatctgtag 1434  
 ttgccatggg gacagtg 1451

&lt;210&gt; 44

&lt;211&gt; 398

&lt;212&gt; PRT

&lt;213&gt; NM\_013952 PAX8

&lt;400&gt; 44

Met Pro His Asn Ser Ile Arg Ser Gly His Gly Gly Leu Asn Gln Leu  
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Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln  
 20 25 30



Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser

35

40

45

Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg  
50 55 60

Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys  
65 70 75 80

Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys  
85 90 95

Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu  
100 105 110

Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile  
115 120 125

Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met  
130 135 140

Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile  
145 150 155 160

Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu  
165 170 175

Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly  
180 185 190

Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu  
195 200 205

Ser Ile Asp Ser Gln Ser Ser Ser Ser Gly Pro Arg Lys His Leu Arg  
210 215 220

Thr Asp Ala Phe Ser Gln His His Leu Glu Pro Leu Glu Cys Pro Phe  
225 230 235 240

Glu Arg Gln His Tyr Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys  
245 250 255

Gly Glu Gln Gly Leu Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp  
260 265 270

Asp Gly Lys Ala Thr Leu Thr Pro Ser Asn Thr Pro Leu Gly Arg Asn  
275 280 285

Leu Ser Thr His Gln Thr Tyr Pro Val Val Ala Ala Pro Pro Phe Trp  
290 295 300

Ile Cys Ser Lys Ser Ala Pro Gly Ser Arg Pro Ser Met Pro Phe Pro  
 305 310 315 320

Met Leu Pro Pro Cys Thr Gly Ser Ser Arg Ala Arg Pro Ser Ser Gln  
 325 330 335

Gly Glu Arg Trp Trp Gly Pro Arg Cys Pro Asp Thr His Pro Thr Ser  
 340 345 350

Pro Pro Ala Asp Arg Ala Ala Met Pro Pro Leu Pro Ser Gln Ala Trp  
 355 360 365

Trp Gln Glu Val Asn Thr Leu Ala Met Pro Met Ala Thr Pro Pro Thr  
 370 375 380

Pro Pro Thr Ala Arg Pro Gly Ala Ser Pro Thr Pro Ala Cys  
 385 390 395

<210> 45

<211> 326

<212> DNA

<213> AI301558 EST

<400> 45

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 gcagggtggtt gcggtcacia agagaaatca tcaagaatgt tcacttggca tgtgtgaaag 180  
 attcaggggg tctgcagctg tttagtgttg atgcagttgg gtcaaaagag tatcatgtta 240  
 gtcttctgtg gggttttaggg agggattatg gagcctccct cccacccac tggctttctt 300  
 gtgtcacagc ctttatttct actccg 326

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<211> 1534

<212> DNA

<213> NM\_018000 FLJ10116

<220>

<221> CDS

<222> (267)..(938)

<223>

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 gtgatgcgcg cggaccagcc cgcgacgccc gggctgccgc tgtccccgca cctggacgct 180  
 ggcgcggttg ccgcgccccca gctcgatcg ctgcgcgagg cgactcggcc ccaggcttcc 240  
 ggcgcggttg ggggccctcg ctctcc atg ggg ctg agg gac tgg ctg aga acc 293  
 Met Gly Leu Arg Asp Trp Leu Arg Thr  
 1 5  
 gtg tgc tgc tgc tgc cgg tgc gag tgc ttg gag gag cgc gcc ctg cct 341  
 Val Cys Cys Cys Cys Arg Cys Glu Cys Leu Glu Glu Arg Ala Leu Pro  
 10 15 20 25  
 gag aag gag ccc ctc gtc agt gat aac aat cca tat tcc tca ttt gga 389  
 Glu Lys Glu Pro Leu Val Ser Asp Asn Asn Pro Tyr Ser Ser Phe Gly  
 30 35 40  
 gca act ctg gtg agg gat gat gag aag aat tta tgg agt atg ccc cat 437  
 Ala Thr Leu Val Arg Asp Asp Glu Lys Asn Leu Trp Ser Met Pro His  
 45 50 55  
 gat gtg tcc cac aca gag gca gac gac gac aga acc ctg tac aat ttg 485  
 Asp Val Ser His Thr Glu Ala Asp Asp Asp Arg Thr Leu Tyr Asn Leu  
 60 65 70  
 ata gtc att cgt aat cag cag gcc aaa gac tca gag gag tgg cag aag 533  
 Ile Val Ile Arg Asn Gln Gln Ala Lys Asp Ser Glu Glu Trp Gln Lys  
 75 80 85  
 ctc aac tat gat atc cat acc ctg cgg cag gtt cga agg gaa gta aga 581  
 Leu Asn Tyr Asp Ile His Thr Leu Arg Gln Val Arg Arg Glu Val Arg  
 90 95 100 105  
 aac aga tgg aag tgc atc tta gaa gat tta ggt ttt caa aag gaa gct 629  
 Asn Arg Trp Lys Cys Ile Leu Glu Asp Leu Gly Phe Gln Lys Glu Ala  
 110 115 120  
 gac tct ttg ttg tca gtg act aaa ctc agc acc atc agt gat tct aaa 677  
 Asp Ser Leu Leu Ser Val Thr Lys Leu Ser Thr Ile Ser Asp Ser Lys  
 125 130 135  
 aac aca agg aaa gct cga gag atg ttg tta aaa ctg gct gaa gaa acc 725  
 Asn Thr Arg Lys Ala Arg Glu Met Leu Leu Lys Leu Ala Glu Glu Thr  
 140 145 150  
 agt att ttc cca aca agt tgg gag ctc tca gag aga tat ctc ttt gtt 773  
 Ser Ile Phe Pro Thr Ser Trp Glu Leu Ser Glu Arg Tyr Leu Phe Val  
 155 160 165  
 gtg gac cgt ctc att gca ctt gat gct gca gaa gag ttc ttt aag ctt 821  
 Val Asp Arg Leu Ile Ala Leu Asp Ala Ala Glu Glu Phe Phe Lys Leu  
 170 175 180 185  
 gct cgt cga act tac ccc aag aag cct ggg gtt cca tgc ctg gca gat 869  
 Ala Arg Arg Thr Tyr Pro Lys Lys Pro Gly Val Pro Cys Leu Ala Asp  
 190 195 200  
 ggc cag aaa gaa ctg cac ctg tgg ggg gac ctc tca tgc aga ctt gca 917  
 Gly Gln Lys Glu Leu His Leu Trp Gly Asp Leu Ser Cys Arg Leu Ala  
 205 210 215  
 cat atg cag gga gta ttg cac tgaagatctt tgctggacct tcttctcttc 968

His Met Gln Gly Val Leu His  
220

agaagataat tttcaaaagg gagcaatgct gtgaatgcag cttgcttctc tctacagatt 1028  
gagaagtcca gcttcaaaag ttacttgcca cttaagcaag gaacttgtca agagatcatg 1088  
gttcatgtta ctgaaaagac ttttaaggatt tgtaaggtta atccatagat tgctgagaac 1148  
aatggaaata tttttatttt tacagatttt gcacttctga attcaggtta aaaactaact 1208  
tgtatttagt ctgcttagag gactgtgact tgaaaatttt tatataccaa tgagcttttt 1268  
ggtagcgtcc acaatgttta aaatatttca taggcgagat ccgtgttctc catttattaa 1328  
tgcattgtag accaatttaa ctgctgtgtt tcaggaaaat tcttcctagt ttaataagca 1388  
agctaaaagt tttatttttt atatttagtg cttaatcttt gcctcatgtt atgtaaaatt 1448  
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aaacaaacaa taaaataaat aaacct 1534

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<211> 224

<212> PRT

<213> NM\_018000 FLJ10116

<400> 47

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Glu Cys Leu Glu Glu Arg Ala Leu Pro Glu Lys Glu Pro Leu Val Ser  
20 25 30

Asp Asn Asn Pro Tyr Ser Ser Phe Gly Ala Thr Leu Val Arg Asp Asp  
35 40 45

Glu Lys Asn Leu Trp Ser Met Pro His Asp Val Ser His Thr Glu Ala  
50 55 60

Asp Asp Asp Arg Thr Leu Tyr Asn Leu Ile Val Ile Arg Asn Gln Gln  
65 70 75 80

Ala Lys Asp Ser Glu Glu Trp Gln Lys Leu Asn Tyr Asp Ile His Thr  
85 90 95

Leu Arg Gln Val Arg Arg Glu Val Arg Asn Arg Trp Lys Cys Ile Leu  
100 105 110

Glu Asp Leu Gly Phe Gln Lys Glu Ala Asp Ser Leu Leu Ser Val Thr  
115 120 125

125

Lys Leu Ser Thr Ile Ser Asp Ser Lys Asn Thr Arg Lys Ala Arg Glu  
130 135 140

Met Leu Leu Lys Leu Ala Glu Glu Thr Ser Ile Phe Pro Thr Ser Trp  
145 150 155 160

Glu Leu Ser Glu Arg Tyr Leu Phe Val Val Asp Arg Leu Ile Ala Leu  
165 170 175

Asp Ala Ala Glu Glu Phe Phe Lys Leu Ala Arg Arg Thr Tyr Pro Lys  
180 185 190

Lys Pro Gly Val Pro Cys Leu Ala Asp Gly Gln Lys Glu Leu His Leu  
195 200 205

Trp Gly Asp Leu Ser Cys Arg Leu Ala His Met Gln Gly Val Leu His  
210 215 220

<210> 48

<211> 2385

<212> DNA

<213> NM\_144724 FLJ30532

<220>

<221> CDS

<222> (71)..(1441)

<223>

<400> 48

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aaaatcacaa atg tca aat gat gga aga tcc agg aat cgg gac agg cgc 109  
Met Ser Asn Asp Gly Arg Ser Arg Asn Arg Asp Arg Arg  
1 5 10

tac gat gag gtc cca agc gac ctg ccc tat caa gat acc acc ata aga 157  
Tyr Asp Glu Val Pro Ser Asp Leu Pro Tyr Gln Asp Thr Thr Ile Arg  
15 20 25

acc cac cca att ctt cat gac agt gag cgg gca gtg agc gct gat ccc 205  
Thr His Pro Ile Leu His Asp Ser Glu Arg Ala Val Ser Ala Asp Pro  
30 35 40 45

ttg cca cca ccc cct ctc cca tta cag cca cca ttc ggc cca gac ttc 253  
Leu Pro Pro Pro Leu Pro Leu Gln Pro Pro Phe Gly Pro Asp Phe  
50 55 60

tac tca agt gac aca gaa gaa cca gct ata gcg cca gat ctc aaa cca 301  
Tyr Ser Ser Asp Thr Glu Glu Pro Ala Ile Ala Pro Asp Leu Lys Pro  
65 70 75

gta agg cgc ttt gtc cct gac tcc tgg aag aac ttt ttc aga ggg aag 349

Val	Arg	Arg	Phe	Val	Pro	Asp	Ser	Trp	Lys	Asn	Phe	Phe	Arg	Gly	Lys	
	80						85					90				
aaa	aag	gac	ccc	gaa	tgg	gat	aag	ccg	gtg	tct	gat	atc	agg	tac	atc	397
Lys	Lys	Asp	Pro	Glu	Trp	Asp	Lys	Pro	Val	Ser	Asp	Ile	Arg	Tyr	Ile	
	95					100					105					
tcc	gat	gga	gtg	gag	tgt	tca	cca	cca	gcc	tct	cca	gca	aga	cca	aac	445
Ser	Asp	Gly	Val	Glu	Cys	Ser	Pro	Pro	Ala	Ser	Pro	Ala	Arg	Pro	Asn	
110				115						120					125	
cac	cgt	tcg	ccc	ctc	aac	tcc	tgc	aaa	gat	ccc	tac	gga	ggg	tca	gaa	493
His	Arg	Ser	Pro	Leu	Asn	Ser	Cys	Lys	Asp	Pro	Tyr	Gly	Gly	Ser	Glu	
				130					135					140		
gga	acc	ttt	agt	tcc	cgg	aaa	gag	gct	gac	gca	gtg	ttt	ccc	cgg	gat	541
Gly	Thr	Phe		Ser	Arg	Lys	Glu	Ala	Asp	Ala	Val	Phe	Pro	Arg	Asp	
			145					150					155			
ccc	tat	gga	tct	cta	gac	cga	cac	aca	caa	aca	gtt	cga	aca	tac	agt	589
Pro	Tyr	Gly	Ser	Leu	Asp	Arg	His	Thr	Gln	Thr	Val	Arg	Thr	Tyr	Ser	
		160					165					170				
gag	aag	gtg	gag	gag	tat	aac	ctg	aga	tac	tcc	tac	atg	aag	tcg	tgg	637
Glu	Lys	Val	Glu	Glu	Tyr	Asn	Leu	Arg	Tyr	Ser	Tyr	Met	Lys	Ser	Trp	
	175					180					185					
gca	ggc	ctg	ctg	aga	ata	ctg	ggg	gtg	gtg	gag	ctg	ctt	ttg	ggg	gcc	685
Ala	Gly	Leu	Leu	Arg	Ile	Leu	Gly	Val	Val	Glu	Leu	Leu	Leu	Gly	Ala	
190					195					200					205	
ggg	gtc	ttt	gct	tgt	gtc	aca	gct	tac	att	cac	aag	gac	agt	gag	tgg	733
Gly	Val	Phe	Ala	Cys	Val	Thr	Ala	Tyr	Ile	His	Lys	Asp	Ser	Glu	Trp	
				210					215					220		
tac	aac	ttg	ttt	gga	tat	tca	caa	ccg	tat	ggc	atg	gga	ggc	gtt	ggg	781
Tyr	Asn	Leu		Phe	Gly	Tyr	Ser	Gln	Pro	Tyr	Gly	Met	Gly	Gly	Val	
			225						230					235		
gga	ttg	ggc	agt	atg	tat	ggg	ggc	tat	tac	tac	act	ggc	cct	aag	acc	829
Gly	Leu	Gly	Ser	Met	Tyr	Gly	Gly	Tyr	Tyr	Tyr	Thr	Gly	Pro	Lys	Thr	
		240					245					250				
cct	ttt	gta	ctc	gtg	gtt	gct	gga	tta	gct	tgg	atc	acc	acc	att	att	877
Pro	Phe	Val	Leu	Val	Val	Ala	Gly	Leu	Ala	Trp	Ile	Thr	Thr	Ile	Ile	
		255				260					265					
att	ctg	gtt	ctt	ggc	atg	tcc	atg	tat	tac	cgg	acc	att	ctt	ctg	gac	925
Ile	Leu	Val	Leu	Gly	Met	Ser	Met	Tyr	Tyr	Arg	Thr	Ile	Leu	Leu	Asp	
270					275					280					285	
tct	aat	tgg	tgg	ccc	cta	act	gaa	ttt	gga	att	aac	gtt	gcc	ttg	ttt	973
Ser	Asn	Trp	Trp	Pro	Leu	Thr	Glu	Phe	Gly	Ile	Asn	Val	Ala	Leu	Phe	
				290					295					300		
att	ttg	tat	atg	gcc	gca	gcc	ata	gtc	tat	gtg	aat	gat	acc	aac	cga	1021
Ile	Leu	Tyr	Met	Ala	Ala	Ala	Ile	Val	Tyr	Val	Asn	Asp	Thr	Asn	Arg	
			305					310					315			
ggg	ggc	ctc	tgc	tac	tat	ccg	tta	ttt	aat	aca	cca	gtg	aat	gca	gtg	1069
Gly	Gly	Leu	Cys	Tyr	Tyr	Pro	Leu	Phe	Asn	Thr	Pro	Val	Asn	Ala	Val	
		320					325					330				
ttc	tgc	cgg	gta	gaa	gga	gga	cag	ata	gct	gca	atg	atc	ttc	ctg	ttt	1117
Phe	Cys	Arg	Val	Glu	Gly	Gly	Gln	Ile	Ala	Ala	Met	Ile	Phe	Leu	Phe	
	335					340					345					
gtc	acc	atg	ata	gtt	tat	ctc	att	agt	gct	ttg	gtt	tgc	cta	aag	tta	1165

Val Thr Met Ile Val Tyr Leu Ile Ser Ala Leu Val Cys Leu Lys Leu	
350 355 360 365	
tgg agg cat gag gca gct cgg aga cat aga gaa tat atg gaa caa cag	1213
Trp Arg His Glu Ala Ala Arg Arg His Arg Glu Tyr Met Glu Gln Gln	
370 375 380	
gag ata aat gag cca tca ttg tca tcg aaa agg aaa atg tgt gaa atg	1261
Glu Ile Asn Glu Pro Ser Leu Ser Ser Lys Arg Lys Met Cys Glu Met	
385 390 395	
gcc acc agt ggt gac aga caa aga gac tca gaa gtt aat ttc aag gaa	1309
Ala Thr Ser Gly Asp Arg Gln Arg Asp Ser Glu Val Asn Phe Lys Glu	
400 405 410	
ctg aga aca gca aaa atg aaa cct gaa cta ctg agt gga cac atc ccc	1357
Leu Arg Thr Ala Lys Met Lys Pro Glu Leu Leu Ser Gly His Ile Pro	
415 420 425	
cca cgc cca gct aat ttt ttt gta ttt tta gta gag atg ggg ttt cac	1405
Pro Arg Pro Ala Asn Phe Phe Val Phe Leu Val Glu Met Gly Phe His	
430 435 440 445	
cgt gtt agc cag gat gat ctc gat ctc ctg acc tca tgatccaccc	1451
Arg Val Ser Gln Asp Asp Leu Asp Leu Leu Thr Ser	
450 455	
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gcagggatgc ttcattcttc taagaattat cttggctttg gactttattc ataaatgttt	1931
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tcttgttgga ttttatcag cagcatctat catgtagata aattcccagg tgtagcatta	2051
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gataaaacca aagaaaagca tgtggaaaag cagaagctta gaaagttgtg gtcactgaat	2171
gcactccctg gtttttattt gtcagtgaat tctttatgca ttcattgtta atattttaat	2231
tccatggctt tgtaggctgt gctgtgtctg aaggggtaac acctagggaa acatgaggcc	2291
ccttatggga ccccccaat ggaacaactt cactttctct tttatgtatt gagccctgtg	2351
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&lt;210&gt; 49

&lt;211&gt; 457

&lt;212&gt; PRT

&lt;213&gt; NM\_144724 FLJ30532

&lt;400&gt; 49

Met Ser Asn Asp Gly Arg Ser Arg Asn Arg Asp Arg Arg Tyr Asp Glu  
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Val Pro Ser Asp Leu Pro Tyr Gln Asp Thr Thr Ile Arg Thr His Pro  
20 25 30

Ile Leu His Asp Ser Glu Arg Ala Val Ser Ala Asp Pro Leu Pro Pro  
35 40 45

Pro Pro Leu Pro Leu Gln Pro Pro Phe Gly Pro Asp Phe Tyr Ser Ser  
50 55 60

Asp Thr Glu Glu Pro Ala Ile Ala Pro Asp Leu Lys Pro Val Arg Arg  
65 70 75 80

Phe Val Pro Asp Ser Trp Lys Asn Phe Phe Arg Gly Lys Lys Lys Asp  
85 90 95

Pro Glu Trp Asp Lys Pro Val Ser Asp Ile Arg Tyr Ile Ser Asp Gly  
100 105 110

Val Glu Cys Ser Pro Pro Ala Ser Pro Ala Arg Pro Asn His Arg Ser  
115 120 125

Pro Leu Asn Ser Cys Lys Asp Pro Tyr Gly Gly Ser Glu Gly Thr Phe  
130 135 140

Ser Ser Arg Lys Glu Ala Asp Ala Val Phe Pro Arg Asp Pro Tyr Gly  
145 150 155 160

Ser Leu Asp Arg His Thr Gln Thr Val Arg Thr Tyr Ser Glu Lys Val  
165 170 175

Glu Glu Tyr Asn Leu Arg Tyr Ser Tyr Met Lys Ser Trp Ala Gly Leu  
180 185 190

Leu Arg Ile Leu Gly Val Val Glu Leu Leu Leu Gly Ala Gly Val Phe  
195 200 205

Ala Cys Val Thr Ala Tyr Ile His Lys Asp Ser Glu Trp Tyr Asn Leu  
210 215 220

Phe Gly Tyr Ser Gln Pro Tyr Gly Met Gly Gly Val Gly Gly Leu Gly  
225 230 235 240

Ser Met Tyr Gly Gly Tyr Tyr Tyr Thr Gly Pro Lys Thr Pro Phe Val  
245 250 255



Leu Val Val Ala Gly Leu Ala Trp Ile Thr Thr Ile Ile Ile Leu Val  
260 265 270

Leu Gly Met Ser Met Tyr Tyr Arg Thr Ile Leu Leu Asp Ser Asn Trp  
275 280 285

Trp Pro Leu Thr Glu Phe Gly Ile Asn Val Ala Leu Phe Ile Leu Tyr  
290 295 300

Met Ala Ala Ala Ile Val Tyr Val Asn Asp Thr Asn Arg Gly Gly Leu  
305 310 315 320

Cys Tyr Tyr Pro Leu Phe Asn Thr Pro Val Asn Ala Val Phe Cys Arg  
325 330 335

Val Glu Gly Gly Gln Ile Ala Ala Met Ile Phe Leu Phe Val Thr Met  
340 345 350

Ile Val Tyr Leu Ile Ser Ala Leu Val Cys Leu Lys Leu Trp Arg His  
355 360 365

Glu Ala Ala Arg Arg His Arg Glu Tyr Met Glu Gln Gln Glu Ile Asn  
370 375 380

Glu Pro Ser Leu Ser Ser Lys Arg Lys Met Cys Glu Met Ala Thr Ser  
385 390 395 400

Gly Asp Arg Gln Arg Asp Ser Glu Val Asn Phe Lys Glu Leu Arg Thr  
405 410 415

Ala Lys Met Lys Pro Glu Leu Leu Ser Gly His Ile Pro Pro Arg Pro  
420 425 430

Ala Asn Phe Phe Val Phe Leu Val Glu Met Gly Phe His Arg Val Ser  
435 440 445

Gln Asp Asp Leu Asp Leu Leu Thr Ser  
450 455

<210> 50

<211> 2280

<212> DNA

<213> NM\_006424 SLC34A2

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<221> CDS

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&lt;223&gt;

&lt;400&gt; 50

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 Met Ala Pro Trp Pro Glu Leu Gly Asp Ala Gln Pro Asn Pro Asp  
 1 5 10 15  
 aag tac ctc gaa ggg gcc gca ggt cag cag ccc act gcc cct gat aaa 156  
 Lys Tyr Leu Glu Gly Ala Ala Gly Gln Gln Pro Thr Ala Pro Asp Lys  
 20 25 30  
 agc aaa gag acc aac aaa aca gat aac act gag gca cct gta acc aag 204  
 Ser Lys Glu Thr Asn Lys Thr Asp Asn Thr Glu Ala Pro Val Thr Lys  
 35 40 45  
 att gaa ctt ctg ccg tcc tac tcc acg gct aca ctg ata gat gag ccc 252  
 Ile Glu Leu Leu Pro Ser Tyr Ser Thr Ala Thr Leu Ile Asp Glu Pro  
 50 55 60  
 act gag gtg gat gac ccc tgg aac cta ccc act ctt cag gac tcg ggg 300  
 Thr Glu Val Asp Asp Pro Trp Asn Leu Pro Thr Leu Gln Asp Ser Gly  
 65 70 75  
 atc aag tgg tca gag aga gac acc aaa ggg aag att ctc tgt ttc ttc 348  
 Ile Lys Trp Ser Glu Arg Asp Thr Lys Gly Lys Ile Leu Cys Phe Phe  
 80 85 90 95  
 caa ggg att ggg aga ttg att tta ctt ctc gga ttt ctc tac ttt ttc 396  
 Gln Gly Ile Gly Arg Leu Ile Leu Leu Leu Gly Phe Leu Tyr Phe Phe  
 100 105 110  
 gtg tgc tcc ctg gat att ctt agt agc gcc ttc cag ctg gtt gga gga 444  
 Val Cys Ser Leu Asp Ile Leu Ser Ser Ala Phe Gln Leu Val Gly Gly  
 115 120 125  
 aaa atg gca gga cag ttc ttc agc aac agc tct att atg tcc aac cct 492  
 Lys Met Ala Gly Gln Phe Phe Ser Asn Ser Ser Ile Met Ser Asn Pro  
 130 135 140  
 ttg ttg ggg ctg gtg atc ggg gtg ctg gtg acc gtc ttg gtg cag agc 540  
 Leu Leu Gly Leu Val Ile Gly Val Leu Val Thr Val Leu Val Gln Ser  
 145 150 155  
 tcc agc acc tca acg tcc atc gtt gtc agc atg gtg tcc tct tca ttg 588  
 Ser Ser Thr Ser Thr Ser Ile Val Val Ser Met Val Ser Ser Ser Leu  
 160 165 170 175  
 ctc act gtt cgg gct gcc atc ccc att atc atg ggg gcc aac att gga 636  
 Leu Thr Val Arg Ala Ala Ile Pro Ile Ile Met Gly Ala Asn Ile Gly  
 180 185 190  
 acg tca atc acc aac act att gtt gcg ctc atg cag gtg gga gat cgg 684  
 Thr Ser Ile Thr Asn Thr Ile Val Ala Leu Met Gln Val Gly Asp Arg  
 195 200 205  
 agt gag ttc aga aga gct ttt gca gga gcc act gtc cat gac ttc ttc 732  
 Ser Glu Phe Arg Arg Ala Phe Ala Gly Ala Thr Val His Asp Phe Phe  
 210 215 220  
 aac tgg ctg tcc gtg ttg gtg ctc ttg ccc gtg gag gtg gcc acc cat 780  
 Asn Trp Leu Ser Val Leu Val Leu Leu Pro Val Glu Val Ala Thr His  
 225 230 235

tac ctc gag atc ata acc cag ctt ata gtg gag agc ttc cac ttc aag Tyr Leu Glu Ile Ile Thr Gln Leu Ile Val Glu Ser Phe His Phe Lys 240 245 250 255	828
aat gga gaa gat gcc cca gat ctt ctg aaa gtc atc act aag ccc ttc Asn Gly Glu Asp Ala Pro Asp Leu Leu Lys Val Ile Thr Lys Pro Phe 260 265 270	876
aca aag ctc att gtc cag ctg gat aaa aaa gtt atc agc caa att gca Thr Lys Leu Ile Val Gln Leu Asp Lys Lys Val Ile Ser Gln Ile Ala 275 280 285	924
atg aac gat gaa aaa gcg aaa aac aag agt ctt gtc aag att tgg tgc Met Asn Asp Glu Lys Ala Lys Asn Lys Ser Leu Val Lys Ile Trp Cys 290 295 300	972
aaa act ttt acc aac aag acc cag att aac gtc act gtt ccc tcg act Lys Thr Phe Thr Asn Lys Thr Gln Ile Asn Val Thr Val Pro Ser Thr 305 310 315	1020
gct aac tgc acc tcc cct tcc ctc tgt tgg acg gat ggc atc caa aac Ala Asn Cys Thr Ser Pro Ser Leu Cys Trp Thr Asp Gly Ile Gln Asn 320 325 330 335	1068
tgg acc atg aag aat gtg acc tac aag gag aac atc gcc aaa tgc cag Trp Thr Met Lys Asn Val Thr Tyr Lys Glu Asn Ile Ala Lys Cys Gln 340 345 350	1116
cat atc ttt gtg aat ttc cac ctc ccg gat ctt gct gtg ggc acc atc His Ile Phe Val Asn Phe His Leu Pro Asp Leu Ala Val Gly Thr Ile 355 360 365	1164
ttg ctc ata ctc tcc ctg ctg gtc ctc tgt ggt tgc ctg atc atg att Leu Leu Ile Leu Ser Leu Leu Val Leu Cys Gly Cys Leu Ile Met Ile 370 375 380	1212
gtc aag atc ctg ggc tct gtg ctc aag ggg cag gtc gcc act gtc atc Val Lys Ile Leu Gly Ser Val Leu Lys Gly Gln Val Ala Thr Val Ile 385 390 395	1260
aag aag acc atc aac act gat ttc ccc ttt ccc ttt gca tgg ttg act Lys Lys Thr Ile Asn Thr Asp Phe Pro Phe Pro Phe Ala Trp Leu Thr 400 405 410 415	1308
ggc tac ctg gcc atc ctc gtc ggg gca ggc atg acc ttc atc gta cag Gly Tyr Leu Ala Ile Leu Val Gly Ala Gly Met Thr Phe Ile Val Gln 420 425 430	1356
agc agc tct gtg ttc acg tcg gcc ttg acc ccc ctg att gga atc ggc Ser Ser Ser Val Phe Thr Ser Ala Leu Thr Pro Leu Ile Gly Ile Gly 435 440 445	1404
gtg ata acc att gag agg gct tat cca ctc acg ctg ggc tcc aac atc Val Ile Thr Ile Glu Arg Ala Tyr Pro Leu Thr Leu Gly Ser Asn Ile 450 455 460	1452
ggc acc acc acc acc gcc atc ctg gcc gcc tta gcc agc cct ggc aat Gly Thr Thr Thr Thr Ala Ile Leu Ala Ala Leu Ala Ser Pro Gly Asn 465 470 475	1500
gca ttg agg agt tca ctc cag atc gcc ctg tgc cac ttt ttc ttc aac Ala Leu Arg Ser Ser Leu Gln Ile Ala Leu Cys His Phe Phe Phe Asn 480 485 490 495	1548
atc tcc ggc atc ttg ctg tgg tac ccg atc ccg ttc act cgc ctg ccc Ile Ser Gly Ile Leu Leu Trp Tyr Pro Ile Pro Phe Thr Arg Leu Pro 500 505 510	1596

atc cgc atg gcc aag ggg ctg ggc aac atc tct gcc aag tat cgc tgg 1644  
 Ile Arg Met Ala Lys Gly Leu Gly Asn Ile Ser Ala Lys Tyr Arg Trp  
 515 520 525  
 ttc gcc gtc ttc tac ctg atc atc ttc ttc ttc ctg atc ccg ctg acg 1692  
 Phe Ala Val Phe Tyr Leu Ile Ile Phe Phe Phe Leu Ile Pro Leu Thr  
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 gtg ttt gcc ctc tcg ctg gcc ggc tgg cgg gtg ctg gtt ggt gtc ggg 1740  
 Val Phe Gly Leu Ser Leu Ala Gly Trp Arg Val Leu Val Gly Val Gly  
 545 550 555  
 gtt ccc gtc gtc ttc atc atc atc ctg gta ctg tgc ctc cga ctc ctg 1788  
 Val Pro Val Val Phe Ile Ile Ile Leu Val Leu Cys Leu Arg Leu Leu  
 560 565 570 575  
 cag tct cgc tgc cca cgc gtc ctg ccg aag aaa ctc cag aac tgg aac 1836  
 Gln Ser Arg Cys Pro Arg Val Leu Pro Lys Lys Leu Gln Asn Trp Asn  
 580 585 590  
 ttc ctg ccg ctg tgg atg cgc tcg ctg aag ccc tgg gat gcc gtc gtc 1884  
 Phe Leu Pro Leu Trp Met Arg Ser Leu Lys Pro Trp Asp Ala Val Val  
 595 600 605  
 tcc aag ttc acc ggc tgc ttc cag atg cgc tgc tgc tac tgc tgc cgc 1932  
 Ser Lys Phe Thr Gly Cys Phe Gln Met Arg Cys Cys Tyr Cys Cys Arg  
 610 615 620  
 gtg tgc tgc cgc gcg tgc tgc ttg ctg tgt ggc tgc ccc aag tgc tgc 1980  
 Val Cys Cys Arg Ala Cys Cys Leu Leu Cys Gly Cys Pro Lys Cys Cys  
 625 630 635  
 cgc tgc agc aag tgc tgc gag gac ttg gag gag gcg cag gag ggg cag 2028  
 Arg Cys Ser Lys Cys Cys Glu Asp Leu Glu Glu Ala Gln Glu Gly Gln  
 640 645 650 655  
 gat gtc cct gtc aag gct cct gag acc ttt gat aac ata acc att agc 2076  
 Asp Val Pro Val Lys Ala Pro Glu Thr Phe Asp Asn Ile Thr Ile Ser  
 660 665 670  
 aga gag gct cag ggt gag gtc cct gcc tcg gac tca aag acc gaa tgc 2124  
 Arg Glu Ala Gln Gly Glu Val Pro Ala Ser Asp Ser Lys Thr Glu Cys  
 675 680 685  
 acg gcc ttg taggggacgc ccagattgt cagggatggg gggatgggtcc 2173  
 Thr Ala Leu  
 690  
 ttgagttttg catgctctcc tccctccac ttctgcaccc tttcaccacc tcgaggagat 2233  
 ttgctcccca ttagcgaatg aaattgatgc agtcctaaaa aaaaaaa 2280

&lt;210&gt; 51

&lt;211&gt; 690

&lt;212&gt; PRT

&lt;213&gt; NM\_006424 SLC34A2

&lt;400&gt; 51

Met Ala Pro Trp Pro Glu Leu Gly Asp Ala Gln Pro Asn Pro Asp Lys  
 1 5 10 15

Tyr Leu Glu Gly Ala Ala Gly Gln Gln Pro Thr Ala Pro Asp Lys Ser  
20 25 30

Lys Glu Thr Asn Lys Thr Asp Asn Thr Glu Ala Pro Val Thr Lys Ile  
35 40 45

Glu Leu Leu Pro Ser Tyr Ser Thr Ala Thr Leu Ile Asp Glu Pro Thr  
50 55 60

Glu Val Asp Asp Pro Trp Asn Leu Pro Thr Leu Gln Asp Ser Gly Ile  
65 70 75 80

Lys Trp Ser Glu Arg Asp Thr Lys Gly Lys Ile Leu Cys Phe Phe Gln  
85 90 95

Gly Ile Gly Arg Leu Ile Leu Leu Leu Gly Phe Leu Tyr Phe Phe Val  
100 105 110

Cys Ser Leu Asp Ile Leu Ser Ser Ala Phe Gln Leu Val Gly Gly Lys  
115 120 125

Met Ala Gly Gln Phe Phe Ser Asn Ser Ser Ile Met Ser Asn Pro Leu  
130 135 140

Leu Gly Leu Val Ile Gly Val Leu Val Thr Val Leu Val Gln Ser Ser  
145 150 155 160

Ser Thr Ser Thr Ser Ile Val Val Ser Met Val Ser Ser Ser Leu Leu  
165 170 175

Thr Val Arg Ala Ala Ile Pro Ile Ile Met Gly Ala Asn Ile Gly Thr  
180 185 190

Ser Ile Thr Asn Thr Ile Val Ala Leu Met Gln Val Gly Asp Arg Ser  
195 200 205

Glu Phe Arg Arg Ala Phe Ala Gly Ala Thr Val His Asp Phe Phe Asn  
210 215 220

Trp Leu Ser Val Leu Val Leu Leu Pro Val Glu Val Ala Thr His Tyr  
225 230 235 240

Leu Glu Ile Ile Thr Gln Leu Ile Val Glu Ser Phe His Phe Lys Asn  
245 250 255

Gly Glu Asp Ala Pro Asp Leu Leu Lys Val Ile Thr Lys Pro Phe Thr  
260 265 270

Lys Leu Ile Val Gln Leu Asp Lys Lys Val Ile Ser Gln Ile Ala Met

275                      280                      285  
 Asn Asp Glu Lys Ala Lys Asn Lys Ser Leu Val Lys Ile Trp Cys Lys  
 290                      295                      300  
 Thr Phe Thr Asn Lys Thr Gln Ile Asn Val Thr Val Pro Ser Thr Ala  
 305                      310                      315                      320  
 Asn Cys Thr Ser Pro Ser Leu Cys Trp Thr Asp Gly Ile Gln Asn Trp  
 325                      330                      335  
 Thr Met Lys Asn Val Thr Tyr Lys Glu Asn Ile Ala Lys Cys Gln His  
 340                      345                      350  
 Ile Phe Val Asn Phe His Leu Pro Asp Leu Ala Val Gly Thr Ile Leu  
 355                      360                      365  
 Leu Ile Leu Ser Leu Leu Val Leu Cys Gly Cys Leu Ile Met Ile Val  
 370                      375                      380  
 Lys Ile Leu Gly Ser Val Leu Lys Gly Gln Val Ala Thr Val Ile Lys  
 385                      390                      395                      400  
 Lys Thr Ile Asn Thr Asp Phe Pro Phe Pro Phe Ala Trp Leu Thr Gly  
 405                      410                      415  
 Tyr Leu Ala Ile Leu Val Gly Ala Gly Met Thr Phe Ile Val Gln Ser  
 420                      425                      430  
 Ser Ser Val Phe Thr Ser Ala Leu Thr Pro Leu Ile Gly Ile Gly Val  
 435                      440                      445  
 Ile Thr Ile Glu Arg Ala Tyr Pro Leu Thr Leu Gly Ser Asn Ile Gly  
 450                      455                      460  
 Thr Thr Thr Thr Ala Ile Leu Ala Ala Leu Ala Ser Pro Gly Asn Ala  
 465                      470                      475                      480  
 Leu Arg Ser Ser Leu Gln Ile Ala Leu Cys His Phe Phe Phe Asn Ile  
 485                      490                      495  
 Ser Gly Ile Leu Leu Trp Tyr Pro Ile Pro Phe Thr Arg Leu Pro Ile  
 500                      505                      510  
 Arg Met Ala Lys Gly Leu Gly Asn Ile Ser Ala Lys Tyr Arg Trp Phe  
 515                      520                      525  
 Ala Val Phe Tyr Leu Ile Ile Phe Phe Phe Leu Ile Pro Leu Thr Val  
 530                      535                      540  
 Phe Gly Leu Ser Leu Ala Gly Trp Arg Val Leu Val Gly Val Gly Val

545                      550                      555                      560  
 Pro Val Val Phe Ile Ile Ile Leu Val Leu Cys Leu Arg Leu Leu Gln  
                                  565                      570                      575  
 Ser Arg Cys Pro Arg Val Leu Pro Lys Lys Leu Gln Asn Trp Asn Phe  
                                  580                      585                      590  
 Leu Pro Leu Trp Met Arg Ser Leu Lys Pro Trp Asp Ala Val Val Ser  
                                  595                      600                      605  
 Lys Phe Thr Gly Cys Phe Gln Met Arg Cys Cys Tyr Cys Cys Arg Val  
                                  610                      615                      620  
 Cys Cys Arg Ala Cys Cys Leu Leu Cys Gly Cys Pro Lys Cys Cys Arg  
                                  625                      630                      635                      640  
 Cys Ser Lys Cys Cys Glu Asp Leu Glu Glu Ala Gln Glu Gly Gln Asp  
                                  645                      650                      655  
 Val Pro Val Lys Ala Pro Glu Thr Phe Asp Asn Ile Thr Ile Ser Arg  
                                  660                      665                      670  
 Glu Ala Gln Gly Glu Val Pro Ala Ser Asp Ser Lys Thr Glu Cys Thr  
                                  675                      680                      685  
 Ala Leu  
                                  690

<210> 52

<211> 529

<212> DNA

<213> AW959311, DKFZp434J037, EST

<220>

<221> misc\_feature

<222> (393)..(393)

<223> the residue at position 393 is A, T C or G

<400> 52

ctgtttcttc aatggttctc ttcccttttc catcctccaa acctggcctg agcctcctga      60  
 agttgctgct gtgaatctga aagacttgaa aagcctccac ctgctgtgtg gacttcatct      120  
 caagggggccc agcctcctct ggactccacc ttggacctca gtgactcaga acttctgcct      180  
 ctaagctgct ctaaagtcca gactatggat gtgttctcta ggccttcagg actctagaat      240

gtccatattt atttttatgt tcttggtttt gtgttttagg aaaagtgaat cttgctgttt 300  
 tcaataatgt gaatgctatg ttctgggaaa atccactatg acatctaagt tttgtgtaca 360  
 gagagatatt ttgcaacta ttccacactt ctncacacaac cccccacact ccaactccaca 420  
 ctcttgagtc tctttaccta atggtctcta cctaattggac cctcgtggcc aaaaagtcca 480  
 ttaaaccaga aaggtgattg gaaaaaaaaa aaaaaaaact cgagggggg 529

<210> 53

<211> 2100

<212> DNA

<213> AF111713 JAM1, junctional adhesion molecule 1

<220>

<221> CDS

<222> (287)..(1183)

<223>

<400> 53

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 tggctggaga cggagtttcg ctcttgatgc ccagcaggct ggagtgcgat ggcgcgattt 120  
 cggctcactg caacctctc ctcccagagg tactttctcag ccctctagct ccaactgaga 180  
 acccagccag tcaggaagtc gctacttcgg gaacaccaac caatcagggg gccgtcacct 240  
 gctgaaggag tccttcggcg gctgttgtgt cgggagcctg atcgcg atg ggg aca 295  
 Met Gly Thr  
 1

aag gcg caa gtc gag agg aaa ctg ttg tgc ctc ttc ata ttg gcg atc 343  
 Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile Leu Ala Ile  
 5 10 15

ctg ttg tgc tcc ctg gca ttg ggc agt gtt aca gtg cac tct tct gaa 391  
 Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His Ser Ser Glu  
 20 25 30 35

cct gaa gtc aga att cct gag aat aat cct gtg aag ttg tcc tgt gcc 439  
 Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu Ser Cys Ala  
 40 45 50

tac tcg ggc ttt tct tct ccc cgt gtg gag tgg aag ttt gac caa gga 487  
 Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe Asp Gln Gly  
 55 60 65

gac acc acc aga ctc gtt tgc tat aat aac aag atc aca gct tcc tat 535  
 Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr Ala Ser Tyr  
 70 75 80

gag gac cgg gtg acc ttc ttg cca act ggt atc acc ttc aag tcc gtg 583  
 Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe Lys Ser Val  
 85 90 95



aca cgg gaa gac act ggg aca tac act tgt atg gtc tct gag gaa ggc 631  
 Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser Glu Glu Gly  
 100 105 110 115

ggc aac agc tat ggg gag gtc aag gtc aag ctc atc gtg ctt gtg cct 679  
 Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val Leu Val Pro  
 120 125 130

cca tcc aag cct aca gtt aac atc ccc tcc tct gcc acc att ggg aac 727  
 Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr Ile Gly Asn  
 135 140 145

cgg gca gtg ctg aca tgc tca gaa caa gat ggt tcc cca cct tct gaa 775  
 Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro Pro Ser Glu  
 150 155 160

tac acc tgg ttc aaa gat ggg ata gtg atg cct acg aat ccc aaa agc 823  
 Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn Pro Lys Ser  
 165 170 175

acc cgt gcc ttc agc aac tct tcc tat gtc ctg aat ccc aca aca gga 871  
 Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro Thr Thr Gly  
 180 185 190 195

gag ctg gtc ttt gat ccc ctg tca gcc tct gat act gga gaa tac agc 919  
 Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly Glu Tyr Ser  
 200 205 210

tgt gag gca cgg aat ggg tat ggg aca ccc atg act tca aat gct gtg 967  
 Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser Asn Ala Val  
 215 220 225

cgc atg gaa gct gtg gag cgg aat gtg ggg gtc atc gtg gca gcc gtc 1015  
 Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val Ala Ala Val  
 230 235 240

ctt gta acc ctg att ctc ctg gga atc ttg gtt ttt ggc atc tgg ttt 1063  
 Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly Ile Trp Phe  
 245 250 255

gcc tat agc cga ggc cac ttt gac aga aca aag aaa ggg act tcg agt 1111  
 Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly Thr Ser Ser  
 260 265 270 275

aag aag gtg att tac agc cag cct agt gcc cga agt gaa gga gaa ttc 1159  
 Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu Gly Glu Phe  
 280 285 290

aaa cag acc tcg tca ttc ctg gtg tgagcctggg cggctcaccg cctatcatct 1213  
 Lys Gln Thr Ser Ser Phe Leu Val  
 295

gcatttgcct tactcaggtg ctactggact ctggcccctg atgtctgtag tttcacagga 1273

tgccttattt gtcttctaca cccacaggg cccctactt cttcggatgt gtttttaata 1333

atgtcagcta tgtgcccacat cctccttcat gccctccctc cctttcctac cactgctgag 1393

tggcctggaa cttgtttaaa gtgtttattc cccatttctt tgagggatca ggaaggaatc 1453

ctgggtatgc cattgacttc ccttctaagt agacagcaaa aatggcgggg gtcgcaggaa 1513

tctgcactca actgccacc tggctggcag ggatctttga ataggtatct tgagcttggt 1573

tctgggctct ttccttgtgt actgacgacc agggccagct gttctagagt gggaattaga 1633

ggctagagcg gctgaaatgg ttgtttgggtg atgacaactgg ggtccttcca tctctggggc 1693

ccactctctt ctgtcttccc atgggaagtg ccactgggat ccctctgccc tgtcctcctg 1753  
 aatacaagct gactgacatt gactgtgtct gtggaaaatg ggagctcttg ttgtggagag 1813  
 catagtaaat tttcagagaa cttgaagcga aaaggattta aaaccgctgc tctaaagaaa 1873  
 agaaaaactgg aggctgggag cagtgggtca cgctgtgaat cccagaggct gaggcaggcg 1933  
 gatcacctga ggtcgggagt tctggatcag cctgaccaac atggagaaac cctgctggaa 1993  
 atacagagtt agccaggcat ggtgggtgat gcctgtagtc ccagctgctc aggagcctgg 2053  
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<211> 299

<212> PRT

<213> AF111713 JAM1, junctional adhesion molecule 1

<400> 54

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Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His  
 20 25 30

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu  
 35 40 45

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe  
 50 55 60

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr  
 65 70 75 80

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe  
 85 90 95

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser  
 100 105 110

Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val  
 115 120 125

Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr  
 130 135 140

Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro  
 145 150 155 160

Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn  
 165 170 175

Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro  
 180 185 190

Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly  
 195 200 205

Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser  
 210 215 220

Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val  
 225 230 235 240

Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly  
 245 250 255

Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly  
 260 265 270

Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu  
 275 280 285

Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val  
 290 295

<210> 55

<211> 2154

<212> DNA

<213> NM\_006636 MTHFD2, methylene tetrahydrofolate

<220>

<221> CDS

<222> (77)..(1108)

<223>

<400> 55

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ggctgcgact tctcta atg tct gct ttg gct gcc cgg ctg ctg cag ccc gcg 112  
 Met Ser Ala Leu Ala Ala Arg Leu Leu Gln Pro Ala  
 1 5 10

cac agc tgc tcc ctt cgc ctt cgc cct ttc cac ctc gcg gca gtt cga 160  
 His Ser Cys Ser Leu Arg Leu Arg Pro Phe His Leu Ala Ala Val Arg  
 15 20 25

aat gaa gct gtt gtc att tct gga agg aaa ctg gcc cag cag atc aag Asn Glu Ala Val Val Ile Ser Gly Arg Lys Leu Ala Gln Gln Ile Lys 30 35 40	208
cag gaa gtg cgg cag gag gta gaa gag tgg gtg gcc tca ggc aac aaa Gln Glu Val Arg Gln Glu Val Glu Glu Trp Val Ala Ser Gly Asn Lys 45 50 55 60	256
cgg cca cac ctg agt gtg atc ctg gtt ggc gag aat cct gca agt cac Arg Pro His Leu Ser Val Ile Leu Val Gly Glu Asn Pro Ala Ser His 65 70 75	304
tcc tat gtc ctc aac aaa acc agg gca gct gca gtt gtg gga atc aac Ser Tyr Val Leu Asn Lys Thr Arg Ala Ala Ala Val Val Gly Ile Asn 80 85 90	352
agt gag aca att atg aaa cca gct tca att tca gag gaa gaa ttg ttg Ser Glu Thr Ile Met Lys Pro Ala Ser Ile Ser Glu Glu Glu Leu Leu 95 100 105	400
aat tta atc aat aaa ctg aat aat gat gat aat gta gat ggc ctc ctt Asn Leu Ile Asn Lys Leu Asn Asn Asp Asp Asn Val Asp Gly Leu Leu 110 115 120	448
gtt cag ttg cct ctt cca gag cat att gat gag aga agg atc tgc aat Val Gln Leu Pro Leu Pro Glu His Ile Asp Glu Arg Arg Ile Cys Asn 125 130 135 140	496
gct gtt tct cca gac aag gat gtt gat ggc ttt cat gta att aat gta Ala Val Ser Pro Asp Lys Asp Val Asp Gly Phe His Val Ile Asn Val 145 150 155	544
gga cga atg tgt ttg gat cag tat tcc atg tta ccg gct act cca tgg Gly Arg Met Cys Leu Asp Gln Tyr Ser Met Leu Pro Ala Thr Pro Trp 160 165 170	592
ggg gtg tgg gaa ata atc aag cga act ggc att cca acc cta ggg aag Gly Val Trp Glu Ile Ile Lys Arg Thr Gly Ile Pro Thr Leu Gly Lys 175 180 185	640
aat gtg gtt gtg gct gga agg tca aaa aac gtt gga atg ccc att gca Asn Val Val Val Ala Gly Arg Ser Lys Asn Val Gly Met Pro Ile Ala 190 195 200	688
atg tta ctg cac aca gat ggg gcg cat gaa cgt ccc gga ggt gat gcc Met Leu Leu His Thr Asp Gly Ala His Glu Arg Pro Gly Gly Asp Ala 205 210 215 220	736
act gtt aca ata tct cat cga tat act ccc aaa gag cag ttg aag aaa Thr Val Thr Ile Ser His Arg Tyr Thr Pro Lys Glu Gln Leu Lys Lys 225 230 235	784
cat aca att ctt gca gat att gta ata tct gct gca ggt att cca aat His Thr Ile Leu Ala Asp Ile Val Ile Ser Ala Ala Gly Ile Pro Asn 240 245 250	832
ctg atc aca gca gat atg atc aag gaa gga gca gca gtc att gat gtg Leu Ile Thr Ala Asp Met Ile Lys Glu Gly Ala Ala Val Ile Asp Val 255 260 265	880
gga ata aat aga gtt cac gat cct gta act gcc aaa ccc aag ttg gtt Gly Ile Asn Arg Val His Asp Pro Val Thr Ala Lys Pro Lys Leu Val 270 275 280	928
gga gat gtg gat ttt gaa gga gtc aga caa aaa gct ggg tat atc act Gly Asp Val Asp Phe Glu Gly Val Arg Gln Lys Ala Gly Tyr Ile Thr 285 290 295 300	976

cca gtt cct gga ggt gtt ggc ccc atg aca gtg gca atg cta atg aag 1024  
 Pro Val Pro Gly Gly Val Gly Pro Met Thr Val Ala Met Leu Met Lys  
                     305                    310                    315

aat acc att att gct gca aaa aag gtg ctg agg ctt gaa gag cga gaa 1072  
 Asn Thr Ile Ile Ala Ala Lys Lys Val Leu Arg Leu Glu Glu Arg Glu  
                     320                    325                    330

gtg ctg aag tct aaa gag ctt ggg gta gcc act aat taactactgt 1118  
 Val Leu Lys Ser Lys Glu Leu Gly Val Ala Thr Asn  
                     335                    340

gtcttctgtg tcacaaacag cactccaggc cagctcaaga agcaaagcag gccaatagaa 1178

atgcaatatt ttttaatttat tctactgaaa tgggtttaaaa tgatgccttg tatttattga 1238

aagcttaaat ggggtgggtgt ttctgcacat acctctgcag tacctcacca gggagcattc 1298

cagtatcatg cagggtcctg tgatctagcc aggagcagcc attaacctag tgattaatat 1358

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aggtaccaga ccttttgagt tcaactgatc aaaccaaagg aaaagtgttg ctagagaaaa 1538

ttggggaaaa ggtgaaaaag aaaaaatggt agtaattgag cagaaaaaaa ttaatttata 1598

tatgtattga ttggcaacca gatttatcta agtagaactg aattggctag gaaaaaagaa 1658

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aaatgtttag gattattcct tgctattagt actcatttta tgtatgttac ccttcagtaa 1778

gttctcccca ttttagtttt ctaggactga aaggattcct ttctacatta tacatgtgtg 1838

ttgtcatatt tggcttttgc tatatacttt aacttcattg ttaaattttt gtattgtata 1898

gtttcttttg tgatatctaa aacctatttt tgaaaaacaa acttggttg ataatcattt 1958

gggcagcttg ggtaagtacg caacttaact ttccacaaa gaactgtcag cagctgcctg 2018

cttttctgtg atgtatgtat cctgttgact tttccagaaa ttttttaaga gtttgagtta 2078

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tctgtctggg atggta 2154

&lt;210&gt; 56

&lt;211&gt; 344

&lt;212&gt; PRT

&lt;213&gt; NM\_006636 MTHFD2, methylene tetrahydrofolate

&lt;400&gt; 56

Met Ser Ala Leu Ala Ala Arg Leu Leu Gln Pro Ala His Ser Cys Ser  
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Leu Arg Leu Arg Pro Phe His Leu Ala Ala Val Arg Asn Glu Ala Val  
                     20                    25                    30

Val Ile Ser Gly Arg Lys Leu Ala Gln Gln Ile Lys Gln Glu Val Arg  
35 40 45

Gln Glu Val Glu Glu Trp Val Ala Ser Gly Asn Lys Arg Pro His Leu  
50 55 60

Ser Val Ile Leu Val Gly Glu Asn Pro Ala Ser His Ser Tyr Val Leu  
65 70 75 80

Asn Lys Thr Arg Ala Ala Ala Val Val Gly Ile Asn Ser Glu Thr Ile  
85 90 95

Met Lys Pro Ala Ser Ile Ser Glu Glu Glu Leu Leu Asn Leu Ile Asn  
100 105 110

Lys Leu Asn Asn Asp Asp Asn Val Asp Gly Leu Leu Val Gln Leu Pro  
115 120 125

Leu Pro Glu His Ile Asp Glu Arg Arg Ile Cys Asn Ala Val Ser Pro  
130 135 140

Asp Lys Asp Val Asp Gly Phe His Val Ile Asn Val Gly Arg Met Cys  
145 150 155 160

Leu Asp Gln Tyr Ser Met Leu Pro Ala Thr Pro Trp Gly Val Trp Glu  
165 170 175

Ile Ile Lys Arg Thr Gly Ile Pro Thr Leu Gly Lys Asn Val Val Val  
180 185 190

Ala Gly Arg Ser Lys Asn Val Gly Met Pro Ile Ala Met Leu Leu His  
195 200 205

Thr Asp Gly Ala His Glu Arg Pro Gly Gly Asp Ala Thr Val Thr Ile  
210 215 220

Ser His Arg Tyr Thr Pro Lys Glu Gln Leu Lys Lys His Thr Ile Leu  
225 230 235 240

Ala Asp Ile Val Ile Ser Ala Ala Gly Ile Pro Asn Leu Ile Thr Ala  
245 250 255

Asp Met Ile Lys Glu Gly Ala Ala Val Ile Asp Val Gly Ile Asn Arg  
260 265 270

Val His Asp Pro Val Thr Ala Lys Pro Lys Leu Val Gly Asp Val Asp  
275 280 285

Phe Glu Gly Val Arg Gln Lys Ala Gly Tyr Ile Thr Pro Val Pro Gly  
290 295 300

Gly Val Gly Pro Met Thr Val Ala Met Leu Met Lys Asn Thr Ile Ile  
305 310 315 320

Ala Ala Lys Lys Val Leu Arg Leu Glu Glu Arg Glu Val Leu Lys Ser  
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Lys Glu Leu Gly Val Ala Thr Asn  
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<210> 57

<211> 1117

<212> DNA

<213> NM\_006149 galectin 4, LGALS4

<220>

<221> CDS

<222> (57)..(1025)

<223>

<400> 57

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Ala Tyr Val Pro Ala Pro Gly Tyr Gln Pro Thr Tyr Asn Pro Thr Leu  
5 10 15

cct tac tac cag ccc atc ccg ggc ggg ctc aac gtg gga atg tct gtt 155  
Pro Tyr Tyr Gln Pro Ile Pro Gly Gly Leu Asn Val Gly Met Ser Val  
20 25 30

tac atc caa gga gtg gcc agc gag cac atg aag ccg ttc ttc gtg aac 203  
Tyr Ile Gln Gly Val Ala Ser Glu His Met Lys Arg Phe Phe Val Asn  
35 40 45

ttt gtg gtt ggg cag gat ccg ggc tca gac gtc gcc ttc cac ttc aat 251  
Phe Val Val Gly Gln Asp Pro Gly Ser Asp Val Ala Phe His Phe Asn  
50 55 60 65

ccg ccg ttt gac ggc tgg gac aag gtg gtc ttc aac acg ttg cag ggc 299  
Pro Arg Phe Asp Gly Trp Asp Lys Val Val Phe Asn Thr Leu Gln Gly  
70 75 80

ggg aag tgg ggc agc gag gag agg aag agg agc atg ccc ttc aaa aag 347  
Gly Lys Trp Gly Ser Glu Glu Arg Lys Arg Ser Met Pro Phe Lys Lys  
85 90 95

ggt gcc gcc ttt gag ctg gtc ttc ata gtc ctg gct gag cac tac aag 395  
Gly Ala Ala Phe Glu Leu Val Phe Ile Val Leu Ala Glu His Tyr Lys  
100 105 110

gtg gtg gta aat gga aat ccc ttc tat gag tac ggg cac ccg ctt ccc 443  
Val Val Val Asn Gly Asn Pro Phe Tyr Glu Tyr Gly His Arg Leu Pro

115	120	125	
cta cag atg gtc acc cac ctg caa gtg gat ggg gat ctg caa ctt caa Leu Gln Met Val Thr His Leu Gln Val Asp Gly Asp Leu Gln Leu Gln 130 135 140 145			491
tca atc aac ttc atc gga ggc cag ccc ctg cgg ccc cag gga ccc ccg Ser Ile Asn Phe Ile Gly Gly Gln Pro Leu Arg Pro Gln Gly Pro Pro 150 155 160			539
atg atg cca cct tac cct ggt ccc gga cat tgc cat caa cag ctg aac Met Met Pro Pro Tyr Pro Gly Pro Gly His Cys His Gln Gln Leu Asn 165 170 175			587
agc ctg ccc acc atg gaa gga ccc cca acc ttc aac ccg cct gtg cca Ser Leu Pro Thr Met Glu Gly Pro Pro Thr Phe Asn Pro Pro Val Pro 180 185 190			635
tat ttc ggg agg ctg caa gga ggg ctg aca gct cga aga acc atc atc Tyr Phe Gly Arg Leu Gln Gly Gly Leu Thr Ala Arg Arg Thr Ile Ile 195 200 205			683
atc aag ggc tat gtg cct ccc aca ggc aag agc ttt gct atc aac ttc Ile Lys Gly Tyr Val Pro Pro Thr Gly Lys Ser Phe Ala Ile Asn Phe 210 215 220 225			731
aag gtg ggc tcc tca ggg gac ata gct ctg cac att aat ccc cgc atg Lys Val Gly Ser Ser Gly Asp Ile Ala Leu His Ile Asn Pro Arg Met 230 235 240			779
ggc aac ggt acc gtg gtc cgg aac agc ctt ctg aat ggc tcg tgg gga Gly Asn Gly Thr Val Val Arg Asn Ser Leu Leu Asn Gly Ser Trp Gly 245 250 255			827
tcc gag gag aag aag atc acc cac aac cca ttt ggt ccc gga cag ttc Ser Glu Glu Lys Lys Ile Thr His Asn Pro Phe Gly Pro Gly Gln Phe 260 265 270			875
ttt gat ctg tcc att cgc tgt ggc ttg gat cgc ttc aag gtt tac gcc Phe Asp Leu Ser Ile Arg Cys Gly Leu Asp Arg Phe Lys Val Tyr Ala 275 280 285			923
aat ggc cag cac ctg ttt gac ttt gcc cat cgc ctg tcg gcc ttc cag Asn Gly Gln His Leu Phe Asp Phe Ala His Arg Leu Ser Ala Phe Gln 290 295 300 305			971
agg gtg gac aca ttg gaa atc cag ggt gat gtc acc ttg tcc tat gtc Arg Val Asp Thr Leu Glu Ile Gln Gly Asp Val Thr Leu Ser Tyr Val 310 315 320			1019
cag atc taatctattc ctggggccat aactcatggg aaaacagaat tatccctag Gln Ile			1075

gactcctttc taagccccta ataaaatgtc tgagggtgtc tc 1117

<210> 58

<211> 323

<212> PRT

<213> NM\_006149 galectin 4, LGALS4

<400> 58



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Leu Pro Tyr Tyr Gln Pro Ile Pro Gly Gly Leu Asn Val Gly Met Ser  
20 25 30

Val Tyr Ile Gln Gly Val Ala Ser Glu His Met Lys Arg Phe Phe Val  
35 40 45

Asn Phe Val Val Gly Gln Asp Pro Gly Ser Asp Val Ala Phe His Phe  
50 55 60

Asn Pro Arg Phe Asp Gly Trp Asp Lys Val Val Phe Asn Thr Leu Gln  
65 70 75 80

Gly Gly Lys Trp Gly Ser Glu Glu Arg Lys Arg Ser Met Pro Phe Lys  
85 90 95

Lys Gly Ala Ala Phe Glu Leu Val Phe Ile Val Leu Ala Glu His Tyr  
100 105 110

Lys Val Val Val Asn Gly Asn Pro Phe Tyr Glu Tyr Gly His Arg Leu  
115 120 125

Pro Leu Gln Met Val Thr His Leu Gln Val Asp Gly Asp Leu Gln Leu  
130 135 140

Gln Ser Ile Asn Phe Ile Gly Gly Gln Pro Leu Arg Pro Gln Gly Pro  
145 150 155 160

Pro Met Met Pro Pro Tyr Pro Gly Pro Gly His Cys His Gln Gln Leu  
165 170 175

Asn Ser Leu Pro Thr Met Glu Gly Pro Pro Thr Phe Asn Pro Pro Val  
180 185 190

Pro Tyr Phe Gly Arg Leu Gln Gly Gly Leu Thr Ala Arg Arg Thr Ile  
195 200 205

Ile Ile Lys Gly Tyr Val Pro Pro Thr Gly Lys Ser Phe Ala Ile Asn  
210 215 220

Phe Lys Val Gly Ser Ser Gly Asp Ile Ala Leu His Ile Asn Pro Arg  
225 230 235 240

Met Gly Asn Gly Thr Val Val Arg Asn Ser Leu Leu Asn Gly Ser Trp  
245 250 255

Gly Ser Glu Glu Lys Lys Ile Thr His Asn Pro Phe Gly Pro Gly Gln  
260 265 270

Phe Phe Asp Leu Ser Ile Arg Cys Gly Leu Asp Arg Phe Lys Val Tyr  
 275 280 285

Ala Asn Gly Gln His Leu Phe Asp Phe Ala His Arg Leu Ser Ala Phe  
 290 295 300

Gln Arg Val Asp Thr Leu Glu Ile Gln Gly Asp Val Thr Leu Ser Tyr  
 305 310 315 320

Val Gln Ile

<210> 59

<211> 3697

<212> DNA

<213> NM\_004063 cadherin 17, CDH17

<220>

<221> CDS

<222> (121)..(2616)

<223>

<400> 59  
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 atg ata ctt cag gcc cat ctt cac tcc ctg tgt ctt ctt atg ctt tat 168  
 Met Ile Leu Gln Ala His Leu His Ser Leu Cys Leu Leu Met Leu Tyr  
 1 5 10 15  
 ttg gca act gga tat ggc caa gag ggg aag ttt agt gga ccc ctg aaa 216  
 Leu Ala Thr Gly Tyr Gly Gln Glu Gly Lys Phe Ser Gly Pro Leu Lys  
 20 25 30  
 ccc atg aca ttt tct att tat gaa ggc caa gaa ccg agt caa att ata 264  
 Pro Met Thr Phe Ser Ile Tyr Glu Gly Gln Glu Pro Ser Gln Ile Ile  
 35 40 45  
 ttc cag ttt aag gcc aat cct cct gct gtg act ttt gaa cta act ggg 312  
 Phe Gln Phe Lys Ala Asn Pro Pro Ala Val Thr Phe Glu Leu Thr Gly  
 50 55 60  
 gag aca gac aac ata ttt gtg ata gaa cgg gag gga ctt ctg tat tac 360  
 Glu Thr Asp Asn Ile Phe Val Ile Glu Arg Glu Gly Leu Leu Tyr Tyr  
 65 70 75 80  
 aac aga gcc ttg gac agg gaa aca aga tct act cac aat ctc cag gtt 408  
 Asn Arg Ala Leu Asp Arg Glu Thr Arg Ser Thr His Asn Leu Gln Val  
 85 90 95  
 gca gcc ctg gac gct aat gga att ata gtg gag ggt cca gtc cct atc 456  
 Ala Ala Leu Asp Ala Asn Gly Ile Ile Val Glu Gly Pro Val Pro Ile

100	105	110	
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tca aag tac gaa ggc tca gta agg cag aac tct cgc cca gga aag ccc Ser Lys Tyr Glu Gly Ser Val Arg Gln Asn Ser Arg Pro Gly Lys Pro 130 135 140			552
ttc ttg tat gtc aat gcc aca gac ctg gat gat ccg gcc act ccc aat Phe Leu Tyr Val Asn Ala Thr Asp Leu Asp Asp Pro Ala Thr Pro Asn 145 150 155 160			600
ggc cag ctt tat tac cag att gtc atc cag ctt ccc atg atc aac aat Gly Gln Leu Tyr Tyr Gln Ile Val Ile Gln Leu Pro Met Ile Asn Asn 165 170 175			648
gtc atg tac ttt cag atc aac aac aaa acg gga gcc atc tct ctt acc Val Met Tyr Phe Gln Ile Asn Asn Lys Thr Gly Ala Ile Ser Leu Thr 180 185 190			696
cga gag gga tct cag gaa ttg aat cct gct aag aat cct tcc tat aat Arg Glu Gly Ser Gln Glu Leu Asn Pro Ala Lys Asn Pro Ser Tyr Asn 195 200 205			744
ctg gtg atc tca gtg aag gac atg gga ggc cag agt gag aat tcc ttc Leu Val Ile Ser Val Lys Asp Met Gly Gly Gln Ser Glu Asn Ser Phe 210 215 220			792
agt gat acc aca tct gtg gat atc ata gtg aca gag aat att tgg aaa Ser Asp Thr Thr Ser Val Asp Ile Ile Val Thr Glu Asn Ile Trp Lys 225 230 235 240			840
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atc aaa atc act cag gtg cgg tgg aat gat ccc ggt gca caa tat tcc Ile Lys Ile Thr Gln Val Arg Trp Asn Asp Pro Gly Ala Gln Tyr Ser 260 265 270			936
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gaa gga gat att tac gtg act cag ccc ttg gac cga gaa gaa aag gat Glu Gly Asp Ile Tyr Val Thr Gln Pro Leu Asp Arg Glu Glu Lys Asp 290 295 300			1032
gca tat gtt ttt tat gca gtt gca aag gat gag tac gga aaa cca ctt Ala Tyr Val Phe Tyr Ala Val Ala Lys Asp Glu Tyr Gly Lys Pro Leu 305 310 315 320			1080
tca tat ccg ctg gaa att cat gta aaa gtt aaa gat att aat gat aat Ser Tyr Pro Leu Glu Ile His Val Lys Val Lys Asp Ile Asn Asp Asn 325 330 335			1128
cca cct aca tgt ccg tca cca gta acc gta ttt gag gtc cag gag aat Pro Pro Thr Cys Pro Ser Pro Val Thr Val Phe Glu Val Gln Glu Asn 340 345 350			1176
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gaa gaa aat act gcc aac agt ttt cta aac tac agg att gtg gag caa Glu Glu Asn Thr Ala Asn Ser Phe Leu Asn Tyr Arg Ile Val Glu Gln 1272			

370	375	380	
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gga atg tta cag tta gct aaa cag tcc ttg aag aag caa gat act cct Gly Met Leu Gln Leu Ala Lys Gln Ser Leu Lys Lys Gln Asp Thr Pro 405 410 415			1368
cag tac aac tta acg ata gag gtg tct gac aaa gat ttc aag acc ctt Gln Tyr Asn Leu Thr Ile Glu Val Ser Asp Lys Asp Phe Lys Thr Leu 420 425 430			1416
tgt ttt gtg caa atc aac gtt att gat atc aat gat cag atc ccc atc Cys Phe Val Gln Ile Asn Val Ile Asp Ile Asn Asp Gln Ile Pro Ile 435 440 445			1464
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att ggg tcc acc atc tta acc atc cag gcc act gat gct gat gag cca Ile Gly Ser Thr Ile Leu Thr Ile Gln Ala Thr Asp Ala Asp Glu Pro 465 470 475 480			1560
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gag gga cgc ctg ggg gtt gac aca gat ccc cat acc aac acc gga tat Glu Gly Arg Leu Gly Val Asp Thr Asp Pro His Thr Asn Thr Gly Tyr 500 505 510			1656
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ttt tcc ctc ggc agt gga agc tta caa aac gac tgg gaa gtt tcc aaa Phe Ser Leu Gly Ser Gly Ser Leu Gln Asn Asp Trp Glu Val Ser Lys 705 710 715 720			2280
atc aat ggt act cat gcc cga ctg tct acc agg cac aca gag ttt gag Ile Asn Gly Thr His Ala Arg Leu Ser Thr Arg His Thr Glu Phe Glu 725 730 735			2328
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gaa gga agt tgt ttc cgg cca gca ggt cac cag act ggg ata ccc act Glu Gly Ser Cys Phe Arg Pro Ala Gly His Gln Thr Gly Ile Pro Thr 770 775 780			2472
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gat aat gtt gaa agt gct caa gca tct gaa gtc aaa cct ctg aga agc Asp Asn Val Glu Ser Ala Gln Ala Ser Glu Val Lys Pro Leu Arg Ser 820 825 830			2616
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taaatattct gtacattttt tctttatcaa ggagatatat cagtgttgct tcatagaact			3216
gcctggattc cttttatggt tttctgatt ccactctgtg tccccttcat ccttgactcc			3276

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 tcattcgat gttagtaaag ttttggttat tatatatatta acatgtggaa gaaaacaaga 3636  
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 a 3697

<210> 60

<211> 832

<212> PRT

<213> NM\_004063 cadherin 17, CDH17

<400> 60

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20 25 30

Pro Met Thr Phe Ser Ile Tyr Glu Gly Gln Glu Pro Ser Gln Ile Ile  
35 40 45

Phe Gln Phe Lys Ala Asn Pro Pro Ala Val Thr Phe Glu Leu Thr Gly  
50 55 60

Glu Thr Asp Asn Ile Phe Val Ile Glu Arg Glu Gly Leu Leu Tyr Tyr  
65 70 75 80

Asn Arg Ala Leu Asp Arg Glu Thr Arg Ser Thr His Asn Leu Gln Val  
85 90 95

Ala Ala Leu Asp Ala Asn Gly Ile Ile Val Glu Gly Pro Val Pro Ile  
100 105 110

Thr Ile Glu Val Lys Asp Ile Asn Asp Asn Arg Pro Thr Phe Leu Gln  
115 120 125

Ser Lys Tyr Glu Gly Ser Val Arg Gln Asn Ser Arg Pro Gly Lys Pro  
130 135 140

Phe Leu Tyr Val Asn Ala Thr Asp Leu Asp Asp Pro Ala Thr Pro Asn  
145 150 155 160

Gly Gln Leu Tyr Tyr Gln Ile Val Ile Gln Leu Pro Met Ile Asn Asn  
165 170 175

Val Met Tyr Phe Gln Ile Asn Asn Lys Thr Gly Ala Ile Ser Leu Thr  
180 185 190

Arg Glu Gly Ser Gln Glu Leu Asn Pro Ala Lys Asn Pro Ser Tyr Asn  
195 200 205

Leu Val Ile Ser Val Lys Asp Met Gly Gly Gln Ser Glu Asn Ser Phe  
210 215 220

Ser Asp Thr Thr Ser Val Asp Ile Ile Val Thr Glu Asn Ile Trp Lys  
225 230 235 240

Ala Pro Lys Pro Val Glu Met Val Glu Asn Ser Thr Asp Pro His Pro  
245 250 255

Ile Lys Ile Thr Gln Val Arg Trp Asn Asp Pro Gly Ala Gln Tyr Ser  
260 265 270

Leu Val Asp Lys Glu Lys Leu Pro Arg Phe Pro Phe Ser Ile Asp Gln  
275 280 285

Glu Gly Asp Ile Tyr Val Thr Gln Pro Leu Asp Arg Glu Glu Lys Asp  
290 295 300

Ala Tyr Val Phe Tyr Ala Val Ala Lys Asp Glu Tyr Gly Lys Pro Leu  
305 310 315 320

Ser Tyr Pro Leu Glu Ile His Val Lys Val Lys Asp Ile Asn Asp Asn  
325 330 335

Pro Pro Thr Cys Pro Ser Pro Val Thr Val Phe Glu Val Gln Glu Asn  
340 345 350

Glu Arg Leu Gly Asn Ser Ile Gly Thr Leu Thr Ala His Asp Arg Asp  
355 360 365

Glu Glu Asn Thr Ala Asn Ser Phe Leu Asn Tyr Arg Ile Val Glu Gln  
370 375 380

Thr Pro Lys Leu Pro Met Asp Gly Leu Phe Leu Ile Gln Thr Tyr Ala  
385 390 395 400

Gly Met Leu Gln Leu Ala Lys Gln Ser Leu Lys Lys Gln Asp Thr Pro  
405 410 415

Gln Tyr Asn Leu Thr Ile Glu Val Ser Asp Lys Asp Phe Lys Thr Leu  
420 425 430

Cys Phe Val Gln Ile Asn Val Ile Asp Ile Asn Asp Gln Ile Pro Ile  
 435 440 445  
 Phe Glu Lys Ser Asp Tyr Gly Asn Leu Thr Leu Ala Glu Asp Thr Asn  
 450 455 460  
 Ile Gly Ser Thr Ile Leu Thr Ile Gln Ala Thr Asp Ala Asp Glu Pro  
 465 470 475 480  
 Phe Thr Gly Ser Ser Lys Ile Leu Tyr His Ile Ile Lys Gly Asp Ser  
 485 490 495  
 Glu Gly Arg Leu Gly Val Asp Thr Asp Pro His Thr Asn Thr Gly Tyr  
 500 505 510  
 Val Ile Ile Lys Lys Pro Leu Asp Phe Glu Thr Ala Ala Val Ser Asn  
 515 520 525  
 Ile Val Phe Lys Ala Glu Asn Pro Glu Pro Leu Val Phe Gly Val Lys  
 530 535 540  
 Tyr Asn Ala Ser Ser Phe Ala Lys Phe Thr Leu Ile Val Thr Asp Val  
 545 550 555 560  
 Asn Glu Ala Pro Gln Phe Ser Gln His Val Phe Gln Ala Lys Val Ser  
 565 570 575  
 Glu Asp Val Ala Ile Gly Thr Lys Val Gly Asn Val Thr Ala Lys Asp  
 580 585 590  
 Pro Glu Gly Leu Asp Ile Ser Tyr Ser Leu Arg Gly Asp Thr Arg Gly  
 595 600 605  
 Trp Leu Lys Ile Asp His Val Thr Gly Glu Ile Phe Ser Val Ala Pro  
 610 615 620  
 Leu Asp Arg Glu Ala Gly Ser Pro Tyr Arg Val Gln Val Val Ala Thr  
 625 630 635 640  
 Glu Val Gly Gly Ser Ser Leu Ser Ser Val Ser Glu Phe His Leu Ile  
 645 650 655  
 Leu Met Asp Val Asn Asp Asn Pro Pro Arg Leu Ala Lys Asp Tyr Thr  
 660 665 670  
 Gly Leu Phe Phe Cys His Pro Leu Ser Ala Pro Gly Ser Leu Ile Phe  
 675 680 685  
 Glu Ala Thr Asp Asp Asp Gln His Leu Phe Arg Gly Pro His Phe Thr  
 690 695 700



Phe Ser Leu Gly Ser Gly Ser Leu Gln Asn Asp Trp Glu Val Ser Lys  
705 710 715 720

Ile Asn Gly Thr His Ala Arg Leu Ser Thr Arg His Thr Glu Phe Glu  
725 730 735

Glu Arg Glu Tyr Val Val Leu Ile Arg Ile Asn Asp Gly Gly Arg Pro  
740 745 750

Pro Leu Glu Gly Ile Val Ser Leu Pro Val Thr Phe Cys Ser Cys Val  
755 760 765

Glu Gly Ser Cys Phe Arg Pro Ala Gly His Gln Thr Gly Ile Pro Thr  
770 775 780

Val Gly Met Ala Val Gly Ile Leu Leu Thr Thr Leu Leu Val Ile Gly  
785 790 795 800

Ile Ile Leu Ala Val Val Phe Ile Arg Ile Lys Lys Asp Lys Gly Lys  
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<212> DNA

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<223>

<400> 61

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ctt ttt gcc cac ata gca gct gta ccg att aag cat ctt cct gaa gaa 99  
Leu Phe Ala His Ile Ala Ala Val Pro Ile Lys His Leu Pro Glu Glu  
15 20 25 30

aat gta cat gat gca gat ttt ggt gaa cag aag gat att tca gaa atc 147  
Asn Val His Asp Ala Asp Phe Gly Glu Gln Lys Asp Ile Ser Glu Ile  
35 40 45

aat tta gct gca ggc ttg gac ctc ttt caa ggg gac atc ctc ttg cag 195  
Asn Leu Ala Ala Gly Leu Asp Leu Phe Gln Gly Asp Ile Leu Leu Gln

50	55	60	
aaa tcc aga aat ggc ctg aga gac cca aac acc agg tgg acg ttc ccc Lys Ser Arg Asn Gly Leu Arg Asp Pro Asn Thr Arg Trp Thr Phe Pro 65 70 75			243
att cct tac atc ttg gct gat aat ttg ggg ctg aat gct aaa gga gcc Ile Pro Tyr Ile Leu Ala Asp Asn Leu Gly Leu Asn Ala Lys Gly Ala 80 85 90			291
att ctg tat gcc ttt gag atg ttc cgt ctc aag tcc tgt gtg gat ttc Ile Leu Tyr Ala Phe Glu Met Phe Arg Leu Lys Ser Cys Val Asp Phe 95 100 105 110			339
aag ccc tat gaa gga gag agc tca tat atc ata ttt caa cag ttt gat Lys Pro Tyr Glu Gly Glu Ser Ser Tyr Ile Ile Phe Gln Gln Phe Asp 115 120 125			387
ggg tgc tgg tct gag gtt ggt gac caa cat gtg gga cag aac att tcc Gly Cys Trp Ser Glu Val Gly Asp Gln His Val Gly Gln Asn Ile Ser 130 135 140			435
att ggc caa gga tgt gcc tat aag gcc atc ata gaa cac gag atc ctg Ile Gly Gln Gly Cys Ala Tyr Lys Ala Ile Ile Glu His Glu Ile Leu 145 150 155			483
cat gct ttg gga ttt tac cac gag cag tca agg acg gac cgg gat gat His Ala Leu Gly Phe Tyr His Glu Gln Ser Arg Thr Asp Arg Asp Asp 160 165 170			531
tat gtg aac atc tgg tgg gac caa att ctt tca ggt tac cag cac aac Tyr Val Asn Ile Trp Trp Asp Gln Ile Leu Ser Gly Tyr Gln His Asn 175 180 185 190			579
ttt gac acc tat gat gat agc tta atc aca gac ctc aat aca ccc tat Phe Asp Thr Tyr Asp Asp Ser Leu Ile Thr Asp Leu Asn Thr Pro Tyr 195 200 205			627
gat tat gag tct ttg atg cac tac cag cct ttc tca ttt aac aag aat Asp Tyr Glu Ser Leu Met His Tyr Gln Pro Phe Ser Phe Asn Lys Asn 210 215 220			675
gca agt gtt ccc acc atc aca gcc aag atc cct gag ttt aac tcc att Ala Ser Val Pro Thr Ile Thr Ala Lys Ile Pro Glu Phe Asn Ser Ile 225 230 235			723
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cga atg tac aat tgc acc aca act cac act ctt ttg gac cac tgt act Arg Met Tyr Asn Cys Thr Thr His Thr Leu Leu Asp His Cys Thr 255 260 265 270			819
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act gac tgg gcc cat cag gac agt gct cag gct gga gaa gtg gat cac Thr Asp Trp Ala His Gln Asp Ser Ala Gln Ala Gly Glu Val Asp His 290 295 300			915
acc ttg ttg gga caa tgc aca ggt gcc ggc tac ttc atg cag ttc agc Thr Leu Leu Gly Gln Cys Thr Gly Ala Gly Tyr Phe Met Gln Phe Ser 305 310 315			963
acc agc tcg ggg tcc gcg gaa gag gca gcc cta ctg gag tct cgg att Thr Ser Ser Gly Ser Ala Glu Glu Ala Ala Leu Leu Glu Ser Arg Ile			1011

320	325	330	
ctt tac cca aag agg aag cag cag tgc ctg caa ttt ttc tat aaa atg Leu Tyr Pro Lys Arg Lys Gln Gln Cys Leu Gln Phe Phe Tyr Lys Met 335 340 345 350			1059
acg gga agt cct tca gac aga ctc gtt gtc tgg gtc agg agg gat gac Thr Gly Ser Pro Ser Asp Arg Leu Val Val Trp Val Arg Arg Asp Asp 355 360 365			1107
agc aca ggc aat gtt cgc aag ttg gtg aag gtg cag act ttt caa gga Ser Thr Gly Asn Val Arg Lys Leu Val Lys Val Gln Thr Phe Gln Gly 370 375 380			1155
gat gat gac cac aat tgg aaa att gcc cat gtg gtg ctc aaa gag gaa Asp Asp Asp His Asn Trp Lys Ile Ala His Val Val Leu Lys Glu Glu 385 390 395			1203
cag aag ttt cgc tac ctt ttc cag ggc aca aaa ggc gac cct cag aac Gln Lys Phe Arg Tyr Leu Phe Gln Gly Thr Lys Gly Asp Pro Gln Asn 400 405 410			1251
tca act ggg gga att tac cta gat gac atc act ctg aca gaa acc ccc Ser Thr Gly Gly Ile Tyr Leu Asp Asp Ile Thr Leu Thr Glu Thr Pro 415 420 425 430			1299
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aac acc agc aaa ggg gac aag ctt cag agc cct cga ttc tac aat tcg Asn Thr Ser Lys Gly Asp Lys Leu Gln Ser Pro Arg Phe Tyr Asn Ser 450 455 460			1395
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tct ggt tac ttg aga ctt gct ttt cat gtg tgc agt ggg gag aac gat Ser Gly Tyr Leu Arg Leu Ala Phe His Val Cys Ser Gly Glu Asn Asp 480 485 490			1491
gct atc ctg gag tgg ccg gta gaa aac aga cag gtg ata att acc atc Ala Ile Leu Glu Trp Pro Val Glu Asn Arg Gln Val Ile Ile Thr Ile 495 500 505 510			1539
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tgt ttt aga agc atc gac ttg ggc tgg agt ggt ttc att tcc cac caa Cys Phe Arg Ser Ile Asp Leu Gly Trp Ser Gly Phe Ile Ser His Gln 560 565 570			1731
atg ctg aaa agg agg agt ttc ctg aaa aat gat gac ctc atc ata ttt Met Leu Lys Arg Arg Ser Phe Leu Lys Asn Asp Asp Leu Ile Ile Phe 575 580 585 590			1779
gtg gac ttt gaa gat atc acc cac ctc agc cag act gaa gtt ccc tct Val Asp Phe Glu Asp Ile Thr His Leu Ser Gln Thr Glu Val Pro Ser			1827

595	600	605	
aaa ggc aaa aga ctg agc ccc caa ggc ctc att ctc caa ggc cag gag			1875
Lys Gly Lys Arg Leu Ser Pro Gln Gly Leu Ile Leu Gln Gly Gln Glu			
610	615	620	
cag cag gtc tcc gaa gaa ggt tgc gga aag gcc atg tta gag gaa gcc			1923
Gln Gln Val Ser Glu Glu Gly Ser Gly Lys Ala Met Leu Glu Glu Ala			
625	630	635	
cta cct gtc agc ctg agc cag ggg cag ccc agc cga cag aag cgg tgc			1971
Leu Pro Val Ser Leu Ser Gln Gly Gln Pro Ser Arg Gln Lys Arg Ser			
640	645	650	
gtg gag aac aca ggc ccc ctg gag gac cat aac tgg cca cag tac ttc			2019
Val Glu Asn Thr Gly Pro Leu Glu Asp His Asn Trp Pro Gln Tyr Phe			
655	660	665	670
aga gac cca tgt gac cca aac cct tgc caa aat gac ggc atc tgt gtg			2067
Arg Asp Pro Cys Asp Pro Asn Pro Cys Gln Asn Asp Gly Ile Cys Val			
675	680	685	
aac gtg aag ggg atg gcg agc tgc agg tgc atc tct gga cat gct ttc			2115
Asn Val Lys Gly Met Ala Ser Cys Arg Cys Ile Ser Gly His Ala Phe			
690	695	700	
ttc tac acg ggg gag cgc tgt cag tgc gcc gag gtg cac ggc agt gtc			2163
Phe Tyr Thr Gly Glu Arg Cys Gln Ser Ala Glu Val His Gly Ser Val			
705	710	715	
ctg ggc atg gtg atc gga ggc acg gct ggc gtg atc ttc ttg acc ttc			2211
Leu Gly Met Val Ile Gly Gly Thr Ala Gly Val Ile Phe Leu Thr Phe			
720	725	730	
tcc atc atc gcc atc ctt tcc caa agg cca agg aag tgacctgcct			2257
Ser Ile Ile Ala Ile Leu Ser Gln Arg Pro Arg Lys			
735	740	745	
gctggcattg gccagaccac agcagcacct cctccatgca ggccttaact ttcccatggt			2317
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aaa			2920

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&lt;211&gt; 746

&lt;212&gt; PRT

&lt;213&gt; NM\_005588; meprin A, alpha

&lt;400&gt; 62

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Ala His Ile Ala Ala Val Pro Ile Lys His Leu Pro Glu Glu Asn Val  
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His Asp Ala Asp Phe Gly Glu Gln Lys Asp Ile Ser Glu Ile Asn Leu  
 35 40 45

Ala Ala Gly Leu Asp Leu Phe Gln Gly Asp Ile Leu Leu Gln Lys Ser  
 50 55 60

Arg Asn Gly Leu Arg Asp Pro Asn Thr Arg Trp Thr Phe Pro Ile Pro  
 65 70 75 80

Tyr Ile Leu Ala Asp Asn Leu Gly Leu Asn Ala Lys Gly Ala Ile Leu  
 85 90 95

Tyr Ala Phe Glu Met Phe Arg Leu Lys Ser Cys Val Asp Phe Lys Pro  
 100 105 110

Tyr Glu Gly Glu Ser Ser Tyr Ile Ile Phe Gln Gln Phe Asp Gly Cys  
 115 120 125

Trp Ser Glu Val Gly Asp Gln His Val Gly Gln Asn Ile Ser Ile Gly  
 130 135 140

Gln Gly Cys Ala Tyr Lys Ala Ile Ile Glu His Glu Ile Leu His Ala  
 145 150 155 160

Leu Gly Phe Tyr His Glu Gln Ser Arg Thr Asp Arg Asp Asp Tyr Val  
 165 170 175

Asn Ile Trp Trp Asp Gln Ile Leu Ser Gly Tyr Gln His Asn Phe Asp  
 180 185 190

Thr Tyr Asp Asp Ser Leu Ile Thr Asp Leu Asn Thr Pro Tyr Asp Tyr  
 195 200 205

Glu Ser Leu Met His Tyr Gln Pro Phe Ser Phe Asn Lys Asn Ala Ser  
 210 215 220

Val Pro Thr Ile Thr Ala Lys Ile Pro Glu Phe Asn Ser Ile Ile Gly  
 225 230 235 240

Gln Arg Leu Asp Phe Ser Ala Ile Asp Leu Glu Arg Leu Asn Arg Met  
245 250 255

Tyr Asn Cys Thr Thr Thr His Thr Leu Leu Asp His Cys Thr Phe Glu  
260 265 270

Lys Ala Asn Ile Cys Gly Met Ile Gln Gly Thr Arg Asp Asp Thr Asp  
275 280 285

Trp Ala His Gln Asp Ser Ala Gln Ala Gly Glu Val Asp His Thr Leu  
290 295 300

Leu Gly Gln Cys Thr Gly Ala Gly Tyr Phe Met Gln Phe Ser Thr Ser  
305 310 315 320

Ser Gly Ser Ala Glu Glu Ala Ala Leu Leu Glu Ser Arg Ile Leu Tyr  
325 330 335

Pro Lys Arg Lys Gln Gln Cys Leu Gln Phe Phe Tyr Lys Met Thr Gly  
340 345 350

Ser Pro Ser Asp Arg Leu Val Val Trp Val Arg Arg Asp Asp Ser Thr  
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Gly Asn Val Arg Lys Leu Val Lys Val Gln Thr Phe Gln Gly Asp Asp  
370 375 380

Asp His Asn Trp Lys Ile Ala His Val Val Leu Lys Glu Glu Gln Lys  
385 390 395 400

Phe Arg Tyr Leu Phe Gln Gly Thr Lys Gly Asp Pro Gln Asn Ser Thr  
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Gly Gly Ile Tyr Leu Asp Asp Ile Thr Leu Thr Glu Thr Pro Cys Pro  
420 425 430

Thr Gly Val Trp Thr Val Arg Asn Phe Ser Gln Val Leu Glu Asn Thr  
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Ser Lys Gly Asp Lys Leu Gln Ser Pro Arg Phe Tyr Asn Ser Glu Gly  
450 455 460

Tyr Gly Phe Gly Val Thr Leu Tyr Pro Asn Ser Arg Glu Ser Ser Gly  
465 470 475 480

Tyr Leu Arg Leu Ala Phe His Val Cys Ser Gly Glu Asn Asp Ala Ile  
485 490 495

Leu Glu Trp Pro Val Glu Asn Arg Gln Val Ile Ile Thr Ile Leu Asp  
500 505 510

Gln Glu Pro Asp Val Arg Asn Arg Met Ser Ser Ser Met Val Phe Thr  
 515 520 525

Thr Ser Lys Ser His Thr Ser Pro Ala Ile Asn Asp Thr Val Ile Trp  
 530 535 540

Asp Arg Pro Ser Arg Val Gly Thr Tyr His Thr Asp Cys Asn Cys Phe  
 545 550 555 560

Arg Ser Ile Asp Leu Gly Trp Ser Gly Phe Ile Ser His Gln Met Leu  
 565 570 575

Lys Arg Arg Ser Phe Leu Lys Asn Asp Asp Leu Ile Ile Phe Val Asp  
 580 585 590

Phe Glu Asp Ile Thr His Leu Ser Gln Thr Glu Val Pro Ser Lys Gly  
 595 600 605

Lys Arg Leu Ser Pro Gln Gly Leu Ile Leu Gln Gly Gln Glu Gln Gln  
 610 615 620

Val Ser Glu Glu Gly Ser Gly Lys Ala Met Leu Glu Glu Ala Leu Pro  
 625 630 635 640

Val Ser Leu Ser Gln Gly Gln Pro Ser Arg Gln Lys Arg Ser Val Glu  
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Asn Thr Gly Pro Leu Glu Asp His Asn Trp Pro Gln Tyr Phe Arg Asp  
 660 665 670

Pro Cys Asp Pro Asn Pro Cys Gln Asn Asp Gly Ile Cys Val Asn Val  
 675 680 685

Lys Gly Met Ala Ser Cys Arg Cys Ile Ser Gly His Ala Phe Phe Tyr  
 690 695 700

Thr Gly Glu Arg Cys Gln Ser Ala Glu Val His Gly Ser Val Leu Gly  
 705 710 715 720

Met Val Ile Gly Gly Thr Ala Gly Val Ile Phe Leu Thr Phe Ser Ile  
 725 730 735

Ile Ala Ile Leu Ser Gln Arg Pro Arg Lys  
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<212> DNA

<213> NM\_015902 EDD, hyperplastic discs protein, DD5

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&lt;223&gt;

&lt;400&gt; 63

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                   1               5

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Val His Pro Leu Pro Gly Thr Glu Asp Gln Leu Asn Asp Arg Leu Arg
      10               15               20

gaa gtt tct gag aag ctg aac aaa tat aat tta aac agc cac ccc cct      150
Glu Val Ser Glu Lys Leu Asn Lys Tyr Asn Leu Asn Ser His Pro Pro
      25               30               35

ttg aat gta ttg gaa cag gct act att aaa cag tgt gtg gtg gga cca      198
Leu Asn Val Leu Glu Gln Ala Thr Ile Lys Gln Cys Val Val Gly Pro
      40               45               50               55

aat cat gct gcc ttt ctt ctt gag gat ggt aga gtt tgc agg att ggt      246
Asn His Ala Ala Phe Leu Leu Glu Asp Gly Arg Val Cys Arg Ile Gly
      60               65               70

ttt tca gta cag cca gac aga ttg gaa ttg ggt aaa cct gat aat aat      294
Phe Ser Val Gln Pro Asp Arg Leu Glu Leu Gly Lys Pro Asp Asn Asn
      75               80               85

gat ggg tca aag ttg aac agc aac tgc ggg gca ggg agg acg tca agg      342
Asp Gly Ser Lys Leu Asn Ser Asn Ser Gly Ala Gly Arg Thr Ser Arg
      90               95               100

cct ggt agg aca agc gac tct cca tgg ttt ctc tca ggt tct gag act      390
Pro Gly Arg Thr Ser Asp Ser Pro Trp Phe Leu Ser Gly Ser Glu Thr
      105               110               115

cta ggc agg ctg gca ggc aac acc tta gga agc cgc tgg agt tct gga      438
Leu Gly Arg Leu Ala Gly Asn Thr Leu Gly Ser Arg Trp Ser Ser Gly
      120               125               130               135

gtg ggt gga agt ggt gga gga tcc tct ggt agg tca tca gct gga gct      486
Val Gly Gly Ser Gly Gly Gly Ser Ser Gly Arg Ser Ser Ala Gly Ala
      140               145               150

cga gat tcc cgc cgg cag act cga gtt att cgg aca gga cgg gat cga      534
Arg Asp Ser Arg Arg Gln Thr Arg Val Ile Arg Thr Gly Arg Asp Arg
      155               160               165

ggg tct ggg ctt ttg ggc agt cag ccc cag cca gtt att cca gca tct      582
Gly Ser Gly Leu Leu Gly Ser Gln Pro Gln Pro Val Ile Pro Ala Ser
      170               175               180

gtc att cca gag gag ctg att tca cag gcc caa gtt gtt tta caa ggc      630
Val Ile Pro Glu Glu Leu Ile Ser Gln Ala Gln Val Val Leu Gln Gly
      185               190               195

aaa tcc aga agt gtc att att cga gaa ctt cag aga aca aat ctt gat      678
Lys Ser Arg Ser Val Ile Ile Arg Glu Leu Gln Arg Thr Asn Leu Asp
      200               205               210               215

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gtg aac ctt gct gta aat aat tta ctt agc cgg gat gat gaa gat gga Val Asn Leu Ala Val Asn Asn Leu Leu Ser Arg Asp Asp Glu Asp Gly 220 225 230	726
gat gat ggg gat gat aca gcc agc gaa tct tat ttg cct gga gag gat Asp Asp Gly Asp Asp Thr Ala Ser Glu Ser Tyr Leu Pro Gly Glu Asp 235 240 245	774
ctt atg tct ctc ctt gat gcc gac att cat tct gcc cac cca agt gtc Leu Met Ser Leu Leu Asp Ala Asp Ile His Ser Ala His Pro Ser Val 250 255 260	822
att att gat gca gat gcc atg ttt tct gaa gac att agc tat ttt ggt Ile Ile Asp Ala Asp Ala Met Phe Ser Glu Asp Ile Ser Tyr Phe Gly 265 270 275	870
tac cct tct ttt cgt cgt tca tca ctt tcc agg cta ggc tca tct cga Tyr Pro Ser Phe Arg Arg Ser Ser Leu Ser Arg Leu Gly Ser Ser Arg 280 285 290 295	918
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gct ctg tat tct gaa ctt ctg gct gtc agc agt aaa gga gaa ctt tat Ala Leu Tyr Ser Glu Leu Leu Ala Val Ser Ser Lys Gly Glu Leu Tyr 380 385 390	1206
cag tgg aaa tgg agt gaa tct gag cct tac aga aat gcc cag aat cct Gln Trp Lys Trp Ser Glu Ser Glu Pro Tyr Arg Asn Ala Gln Asn Pro 395 400 405	1254
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ata gtc ctc ctg tct gca aat agc ata aga gca act gta gct aca gaa Ile Val Leu Leu Ser Ala Asn Ser Ile Arg Ala Thr Val Ala Thr Glu 425 430 435	1350
aat aac aag gtt gct aca tgg gtg gat gaa act tta agt tct gtg gct Asn Asn Lys Val Ala Thr Trp Val Asp Glu Thr Leu Ser Ser Val Ala 440 445 450 455	1398
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cgg ata gtt tct tta cat tgc tgt gcc ctt tac acc tgc gct cag ctg Arg Ile Val Ser Leu His Cys Cys Ala Leu Tyr Thr Cys Ala Gln Leu 475 480 485	1494

gaa aac agt tta tat tgg tgg ggt gta gtt cct ttt agt caa agg aag Glu Asn Ser Leu Tyr Trp Trp Gly Val Val Pro Phe Ser Gln Arg Lys 490 495 500	1542
aaa atg tta gag aaa gct aga gca aaa aat aaa aag cct aaa tcc agt Lys Met Leu Glu Lys Ala Arg Ala Lys Asn Lys Lys Pro Lys Ser Ser 505 510 515	1590
gct ggt att tct tca atg ccg aac atc act gtt ggt acc cag gta tgc Ala Gly Ile Ser Ser Met Pro Asn Ile Thr Val Gly Thr Gln Val Cys 520 525 530 535	1638
ttg aga aat aat cct ctt tat cat gct gga gca gtt gca ttt tca att Leu Arg Asn Asn Pro Leu Tyr His Ala Gly Ala Val Ala Phe Ser Ile 540 545 550	1686
agt gct ggg att cct aaa gtt ggt gtc tta atg gag tca gtt tgg aat Ser Ala Gly Ile Pro Lys Val Gly Val Leu Met Glu Ser Val Trp Asn 555 560 565	1734
atg aat gac agc tgt aga ttt caa ctt aga tct cct gaa agc ttg aaa Met Asn Asp Ser Cys Arg Phe Gln Leu Arg Ser Pro Glu Ser Leu Lys 570 575 580	1782
aac atg gaa aaa gct agc aaa act act gaa gct aag cct gaa agt aag Asn Met Glu Lys Ala Ser Lys Thr Thr Glu Ala Lys Pro Glu Ser Lys 585 590 595	1830
cag gag cca gtg aaa aca gaa atg ggt cct cca cca tct cca gca tcc Gln Glu Pro Val Lys Thr Glu Met Gly Pro Pro Pro Ser Pro Ala Ser 600 605 610 615	1878
acg tgt agt gat gca tcc tca att gcc agc agt gca tca atg cca tac Thr Cys Ser Asp Ala Ser Ser Ile Ala Ser Ser Ala Ser Met Pro Tyr 620 625 630	1926
aaa cga cga cgg tca acc cct gca cca aaa gaa gag gaa aag gtg aat Lys Arg Arg Arg Ser Thr Pro Ala Pro Lys Glu Glu Glu Lys Val Asn 635 640 645	1974
gaa gag cag tgg tct ctt cgg gaa gtg gtt ttt gtg gaa gat gtc aag Glu Glu Gln Trp Ser Leu Arg Glu Val Val Phe Val Glu Asp Val Lys 650 655 660	2022
aat gtt cct gtt ggc aag gtg cta aaa gta gat ggt gcc tat gtt gct Asn Val Pro Val Gly Lys Val Leu Lys Val Asp Gly Ala Tyr Val Ala 665 670 675	2070
gta aaa ttt cca gga acc tcc agt aat act aac tgt cag aac agc tct Val Lys Phe Pro Gly Thr Ser Ser Asn Thr Asn Cys Gln Asn Ser Ser 680 685 690 695	2118
ggt cca gat gct gac cct tct tct ctc ctg cag gat tgt agg tta ctt Gly Pro Asp Ala Asp Pro Ser Ser Leu Leu Gln Asp Cys Arg Leu Leu 700 705 710	2166
aga att gat gaa ttg cag gtt gtc aaa act ggt gga aca ccg aag gtt Arg Ile Asp Glu Leu Gln Val Val Lys Thr Gly Gly Thr Pro Lys Val 715 720 725	2214
ccc gac tgt ttc caa agg act cct aaa aag ctt tgt ata cct gaa aaa Pro Asp Cys Phe Gln Arg Thr Pro Lys Lys Leu Cys Ile Pro Glu Lys 730 735 740	2262
aca gaa ata tta gca gtg aat gta gat tcc aaa ggt gtt cat gct gtt Thr Glu Ile Leu Ala Val Asn Val Asp Ser Lys Gly Val His Ala Val 745 750 755	2310

ctg aag act gga aat tgg gtg cga tac tgt atc ttt gat ctt gct aca Leu Lys Thr Gly Asn Trp Val Arg Tyr Cys Ile Phe Asp Leu Ala Thr 760 765 770 775	2358
gga aaa gca gaa cag gaa aat aat ttt cct aca agc agc att gct ttc Gly Lys Ala Glu Gln Glu Asn Asn Phe Pro Thr Ser Ser Ile Ala Phe 780 785 790	2406
ctt ggt cag aat gag agg aat gta gcc att ttc act gct gga cag gaa Leu Gly Gln Asn Glu Arg Asn Val Ala Ile Phe Thr Ala Gly Gln Glu 795 800 805	2454
tct ccc att att ctt cga gat gga aat ggt acc atc tac cca atg gcc Ser Pro Ile Ile Leu Arg Asp Gly Asn Gly Thr Ile Tyr Pro Met Ala 810 815 820	2502
aaa gat tgc atg gga gga ata agg gat ccc gat tgg ctg gat ctt cca Lys Asp Cys Met Gly Gly Ile Arg Asp Pro Asp Trp Leu Asp Leu Pro 825 830 835	2550
cct att agt agt ctt gga atg ggt gtg cat tct tta ata aat ctt cct Pro Ile Ser Ser Leu Gly Met Gly Val His Ser Leu Ile Asn Leu Pro 840 845 850 855	2598
gcc aat tca aca atc aaa aag aaa gct gct gtt atc atc atg gct gta Ala Asn Ser Thr Ile Lys Lys Lys Ala Ala Val Ile Ile Met Ala Val 860 865 870	2646
gag aaa caa acc tta atg caa cac att ctg cgc tgt gac tat gag gcc Glu Lys Gln Thr Leu Met Gln His Ile Leu Arg Cys Asp Tyr Glu Ala 875 880 885	2694
tgt cga caa tat cta atg aat ctt gag caa gcg gtt gtt tta gag cag Cys Arg Gln Tyr Leu Met Asn Leu Glu Gln Ala Val Val Leu Glu Gln 890 895 900	2742
aat cta cag atg ctg cag aca ttc atc agc cac aga tgt gat gga aat Asn Leu Gln Met Leu Gln Thr Phe Ile Ser His Arg Cys Asp Gly Asn 905 910 915	2790
cga aat att ttg cat gct tgt gta tca gtt tgc ttt cca acc agc aat Arg Asn Ile Leu His Ala Cys Val Ser Val Cys Phe Pro Thr Ser Asn 920 925 930 935	2838
aaa gaa act aaa gaa gaa gag gaa gcg gag cgt tct gaa aga aat aca Lys Glu Thr Lys Glu Glu Glu Ala Glu Arg Ser Glu Arg Asn Thr 940 945 950	2886
ttt gca gaa agg ctt tct gct gtt gag gcc att gca aat gca ata tca Phe Ala Glu Arg Leu Ser Ala Val Glu Ala Ile Ala Asn Ala Ile Ser 955 960 965	2934
gtt gtt tca agt aat ggc cca ggt aat cgg gct gga tca tca agt agc Val Val Ser Ser Asn Gly Pro Gly Asn Arg Ala Gly Ser Ser Ser Ser 970 975 980	2982
cga agt ttg aga tta cgg gaa atg atg aga cgt tcg ttg aga gca gct Arg Ser Leu Arg Leu Arg Glu Met Met Arg Arg Ser Leu Arg Ala Ala 985 990 995	3030
ggt ttg ggt aga cat gaa gct gga gct tca tcc agt gac cac cag Gly Leu Gly Arg His Glu Ala Gly Ala Ser Ser Ser Asp His Gln 1000 1005 1010	3075
gat cca gtt tca ccc ccc ata gct ccc cct agt tgg gtt cct gac Asp Pro Val Ser Pro Pro Ile Ala Pro Pro Ser Trp Val Pro Asp 1015 1020 1025	3120

cct Pro 1030	cct Pro	gcg Ala	atg Met	gat Asp	cct Pro 1035	gat Asp	ggg Gly	gac Asp	att Ile	gat Asp 1040	ttt Phe	atc Ile	ctg Leu	gcc Ala	3165
ccc Pro 1045	gct Ala	gtg Val	gga Gly	tct Ser	ctt Leu 1050	acc Thr	aca Thr	gca Ala	gca Ala	acc Thr 1055	ggg Gly	act Thr	ggg Gly	caa Gln	3210
gga Gly 1060	cca Pro	agc Ser	acc Thr	tcc Ser	act Thr 1065	att Ile	cca Pro	ggg Gly	cct Pro	tcc Ser 1070	aca Thr	gag Glu	cca Pro	tct Ser	3255
gta Val 1075	gta Val	gaa Glu	tcc Ser	aag Lys	gat Asp 1080	cga Arg	aag Lys	gcg Ala	aat Asn	gct Ala 1085	cat His	ttt Phe	ata Ile	ttg Leu	3300
aaa Lys 1090	ttg Leu	tta Leu	tgt Cys	gac Asp	agt Ser 1095	gtg Val	gtt Val	ctc Leu	cag Gln	ccc Pro 1100	tat Tyr	cta Leu	cga Arg	gaa Glu	3345
ctt Leu 1105	ctt Leu	tct Ser	gcc Ala	aag Lys	gat Asp 1110	gca Ala	aga Arg	ggg Gly	atg Met	acc Thr 1115	cca Pro	ttt Phe	atg Met	tca Ser	3390
gct Ala 1120	gta Val	agt Ser	ggc Gly	cga Arg	gct Ala 1125	tat Tyr	cct Pro	gct Ala	gca Ala	att Ile 1130	acc Thr	atc Ile	tta Leu	gaa Glu	3435
act Thr 1135	gct Ala	cag Gln	aaa Lys	att Ile	gca Ala 1140	aaa Lys	gct Ala	gaa Glu	ata Ile	tcc Ser 1145	tca Ser	agt Ser	gaa Glu	aaa Lys	3480
gag Glu 1150	gaa Glu	gat Asp	gta Val	ttc Phe	atg Met 1155	gga Gly	atg Met	gtt Val	tgc Cys	cca Pro 1160	tca Ser	ggg Gly	acc Thr	aac Asn	3525
cct Pro 1165	gat Asp	gac Asp	tct Ser	cct Pro	tta Leu 1170	tat Tyr	gtt Val	tta Leu	tgt Cys	tgt Cys 1175	aat Asn	gac Asp	act Thr	tgc Cys	3570
agt Ser 1180	ttt Phe	aca Thr	tgg Trp	act Thr	gga Gly 1185	gca Ala	gag Glu	cac His	att Ile	aac Asn 1190	cag Gln	gat Asp	att Ile	ttt Phe	3615
gag Glu 1195	tgt Cys	cga Arg	act Thr	tgt Cys	ggc Gly 1200	ttg Leu	ctg Leu	gag Glu	tca Ser	ctg Leu 1205	tgt Cys	tgt Cys	tgt Cys	acg Thr	3660
gaa Glu 1210	tgt Cys	gca Ala	agg Arg	gtt Val	tgt Cys 1215	cat His	aaa Lys	ggg Gly	cat His	gat Asp 1220	tgc Cys	aaa Lys	ctc Leu	aaa Lys	3705
cgg Arg 1225	aca Thr	tca Ser	cca Pro	aca Thr	gcc Ala 1230	tac Tyr	tgt Cys	gat Asp	tgt Cys	tgg Trp 1235	gag Glu	aaa Lys	tgt Cys	aaa Lys	3750
tgt Cys 1240	aaa Lys	act Thr	ctt Leu	att Ile	gct Ala 1245	gga Gly	cag Gln	aaa Lys	tct Ser	gct Ala 1250	cgt Arg	ctt Leu	gat Asp	cta Leu	3795
ctt Leu 1255	tat Tyr	cgc Arg	ctg Leu	ctc Leu	act Thr 1260	gct Ala	act Thr	aat Asn	ctg Leu	gtt Val 1265	act Thr	ctg Leu	cca Pro	aac Asn	3840
agc Ser 1270	agg Arg	gga Gly	gag Glu	cac His	ctc Leu 1275	tta Leu	cta Leu	ttc Phe	tta Leu	gta Val 1280	cag Gln	aca Thr	gtc Val	gca Ala	3885

agg Arg 1285	cag Gln	acg Thr	gtg Val	gag Glu	cat His 1290	tgt Cys	caa Gln	tac Tyr	agg Arg	cca Pro 1295	cct Pro	cga Arg	atc Ile	agg Arg	3930
gaa Glu 1300	gat Asp	cgt Arg	aac Asn	cga Arg	aaa Lys 1305	aca Thr	gcc Ala	agt Ser	cct Pro	gaa Glu 1310	gat Asp	tca Ser	gat Asp	atg Met	3975
cca Pro 1315	gat Asp	cat His	gat Asp	tta Leu	gag Glu 1320	cct Pro	cca Pro	aga Arg	ttt Phe	gcc Ala 1325	cag Gln	ctt Leu	gca Ala	ttg Leu	4020
gag Glu 1330	cgt Arg	gtt Val	cta Leu	cag Gln	gac Asp 1335	tgg Trp	aat Asn	gcc Ala	ttg Leu	aaa Lys 1340	tct Ser	atg Met	att Ile	atg Met	4065
ttt Phe 1345	ggg Gly	tcg Ser	cag Gln	gag Glu	aat Asn 1350	aaa Lys	gac Asp	cct Pro	ctt Leu	agt Ser 1355	gcc Ala	agc Ser	agt Ser	aga Arg	4110
ata Ile 1360	ggc Gly	cat His	ctt Leu	ttg Leu	cca Pro 1365	gaa Glu	gag Glu	caa Gln	gta Val	tac Tyr 1370	ctc Leu	aat Asn	cag Gln	caa Gln	4155
agt Ser 1375	ggc Gly	aca Thr	att Ile	cgg Arg	ctg Leu 1380	gac Asp	tgt Cys	ttc Phe	act Thr	cat His 1385	tgc Cys	ctt Leu	ata Ile	gtt Val	4200
aag Lys 1390	tgt Cys	aca Thr	gca Ala	gat Asp	att Ile 1395	ttg Leu	ctt Leu	tta Leu	gat Asp	act Thr 1400	cta Leu	cta Leu	ggt Gly	aca Thr	4245
cta Leu 1405	gtg Val	aaa Lys	gaa Glu	ctc Leu	caa Gln 1410	aac Asn	aaa Lys	tat Tyr	aca Thr	cct Pro 1415	gga Gly	cgt Arg	aga Arg	gaa Glu	4290
gaa Glu 1420	gct Ala	att Ile	gct Ala	gtg Val	aca Thr 1425	atg Met	agg Arg	ttt Phe	cta Leu	cgt Arg 1430	tca Ser	gtg Val	gca Ala	aga Arg	4335
gtt Val 1435	ttt Phe	gtt Val	att Ile	ctg Leu	agt Ser 1440	gtg Val	gaa Glu	atg Met	gct Ala	tca Ser 1445	tcc Ser	aaa Lys	aag Lys	aaa Lys	4380
aac Asn 1450	aac Asn	ttt Phe	att Ile	cca Pro	cag Gln 1455	cca Pro	att Ile	gga Gly	aaa Lys	tgc Cys 1460	aag Lys	cgt Arg	gta Val	ttc Phe	4425
caa Gln 1465	gca Ala	ttg Leu	cta Leu	cct Pro	tac Tyr 1470	gct Ala	gtg Val	gaa Glu	gaa Glu	ttg Leu 1475	tgc Cys	aac Asn	gta Val	gca Ala	4470
gag Glu 1480	tca Ser	ctg Leu	att Ile	gtt Val	cct Pro 1485	gtc Val	aga Arg	atg Met	ggg Gly	att Ile 1490	gct Ala	cgt Arg	cca Pro	act Thr	4515
gca Ala 1495	cca Pro	ttt Phe	acc Thr	ctg Leu	gct Ala 1500	agt Ser	act Thr	agc Ser	ata Ile	gat Asp 1505	gcc Ala	atg Met	cag Gln	ggc Gly	4560
agt Ser 1510	gaa Glu	gaa Glu	tta Leu	ttt Phe	tca Ser 1515	gtg Val	gaa Glu	cca Pro	cta Leu	cca Pro 1520	cca Pro	cga Arg	cca Pro	tca Ser	4605
tct Ser 1525	gat Asp	cag Gln	tct Ser	agc Ser	agc Ser 1530	tcc Ser	agt Ser	cag Gln	tct Ser	cag Gln 1535	tca Ser	tcc Ser	tac Tyr	atc Ile	4650

atc Ile 1540	agg Arg	aat Asn	cca Pro	cag Gln	cag Gln 1545	agg Arg	cgc Arg	atc Ile	agc Ser	cag Gln 1550	tca Ser	cag Gln	ccc Pro	gtt Val	4695
cgg Arg 1555	ggc Gly	aga Arg	gat Asp	gaa Glu	gaa Glu 1560	cag Gln	gat Asp	gat Asp	att Ile	gtt Val 1565	tca Ser	gca Ala	gat Asp	gtg Val	4740
gaa Glu 1570	gag Glu	gtt Val	gag Glu	gtg Val	gtg Val 1575	gag Glu	ggg Gly	gtg Val	gct Ala	gga Gly 1580	gaa Glu	gag Glu	gat Asp	cat His	4785
cat His 1585	gat Asp	gaa Glu	cag Gln	gaa Glu	gaa Glu 1590	cac His	ggg Gly	gaa Glu	gaa Glu	aat Asn 1595	gct Ala	gag Glu	gca Ala	gag Glu	4830
gga Gly 1600	caa Gln	cat His	gat Asp	gag Glu	cat His 1605	gat Asp	gaa Glu	gac Asp	ggg Gly	agt Ser 1610	gat Asp	atg Met	gag Glu	ctg Leu	4875
gac Asp 1615	ttg Leu	tta Leu	gca Ala	gca Ala	gct Ala 1620	gaa Glu	aca Thr	gaa Glu	agt Ser	gat Asp 1625	agt Ser	gaa Glu	agt Ser	aac Asn	4920
cac His 1630	agc Ser	aac Asn	caa Gln	gat Asp	aat Asn 1635	gct Ala	agt Ser	ggg Gly	cgc Arg	aga Arg 1640	agc Ser	gtt Val	gtc Val	act Thr	4965
gca Ala 1645	gca Ala	act Thr	gct Ala	ggg Gly	tca Ser 1650	gaa Glu	gca Ala	gga Gly	gca Ala	agc Ser 1655	agt Ser	gtt Val	cct Pro	gcc Ala	5010
ttc Phe 1660	ttt Phe	tct Ser	gaa Glu	gat Asp	gat Asp 1665	tct Ser	caa Gln	tcg Ser	aat Asn	gac Asp 1670	tca Ser	agt Ser	gat Ser	tct Ser	5055
gat Asp 1675	agc Ser	agt Ser	agt Ser	agt Ser	cag Gln 1680	agt Ser	gac Asp	gac Asp	ata Ile	gaa Glu 1685	cag Gln	gag Glu	acc Thr	ttt Phe	5100
atg Met 1690	ctt Leu	gat Asp	gag Glu	cca Pro	tta Leu 1695	gaa Glu	aga Arg	acc Thr	aca Thr	aat Asn 1700	agc Ser	tcc Ser	cat His	gcc Ala	5145
aat Asn 1705	ggg Gly	gct Ala	gcc Ala	caa Gln	gct Ala 1710	ccc Pro	cgt Arg	tca Ser	atg Met	cag Gln 1715	tgg Trp	gct Ala	gtc Val	cgc Arg	5190
aac Asn 1720	acc Thr	cag Gln	cat His	cag Gln	cga Arg 1725	gca Ala	gcc Ala	agt Ser	aca Thr	gcc Ala 1730	cct Pro	tcc Ser	agt Ser	aca Thr	5235
tct Ser 1735	aca Thr	cca Pro	gca Ala	gca Ala	agt Ser 1740	tca Ser	gcg Ala	ggg Gly	ttg Leu	att Ile 1745	tat Tyr	att Ile	gat Asp	cct Pro	5280
tca Ser 1750	aac Asn	tta Leu	cgc Arg	cgg Arg	agt Ser 1755	ggg Gly	acc Thr	atc Ile	agt Ser	aca Thr 1760	agt Ser	gct Ala	gca Ala	gct Ala	5325
gca Ala 1765	gca Ala	gct Ala	gct Ala	ttg Leu	gaa Glu 1770	gct Ala	agc Ser	aac Asn	gcc Ala	agc Ser 1775	agt Ser	tac Tyr	cta Leu	aca Thr	5370
tct Ser 1780	gca Ala	agc Ser	agt Ser	tta Leu	gcc Ala 1785	agg Arg	gct Ala	tac Tyr	agc Ser	att Ile 1790	gtc Val	att Ile	aga Arg	caa Gln	5415

atc Ile 1795	tcg Ser	gac Asp	ttg Leu	atg Met	ggc Gly 1800	ctt Leu	att Ile	cct Pro	aag Lys	tat Tyr 1805	aat Asn	cac His	cta Leu	gta Val	5460
tac Tyr 1810	tct Ser	cag Gln	att Ile	cca Pro	gca Ala 1815	gct Ala	gtg Val	aaa Lys	ttg Leu	act Thr 1820	tac Tyr	caa Gln	gat Asp	gca Ala	5505
gta Val 1825	aac Asn	tta Leu	cag Gln	aac Asn	tat Tyr 1830	gta Val	gaa Glu	gaa Glu	aag Lys	ctt Leu 1835	att Ile	ccc Pro	act Thr	tgg Trp	5550
aac Asn 1840	tgg Trp	atg Met	gtc Val	agt Ser	att Ile 1845	atg Met	gat Asp	tct Ser	act Thr	gaa Glu 1850	gct Ala	caa Gln	tta Leu	cgt Arg	5595
tat Tyr 1855	ggc Gly	tct Ser	gca Ala	tta Leu	gca Ala 1860	tct Ser	gct Ala	ggc Gly	gat Asp	cct Pro 1865	gga Gly	cat His	cca Pro	aat Asn	5640
cat His 1870	cct Pro	ctt Leu	cac His	gct Ala	tct Ser 1875	cag Gln	aat Asn	tca Ser	gcg Ala	aga Arg 1880	aga Arg	gag Glu	agg Arg	atg Met	5685
act Thr 1885	gcg Ala	cga Arg	gaa Glu	gaa Glu	gct Ala 1890	agc Ser	tta Leu	cga Arg	aca Thr	ctt Leu 1895	gaa Glu	ggc Gly	aga Arg	cga Arg	5730
cgt Arg 1900	gcc Ala	acc Thr	ttg Leu	ctt Leu	agc Ser 1905	gcc Ala	cgt Arg	caa Gln	gga Gly	atg Met 1910	atg Met	tct Ser	gca Ala	cga Arg	5775
gga Gly 1915	gac Asp	ttc Phe	cta Leu	aat Asn	tat Tyr 1920	gct Ala	ctg Leu	tct Ser	cta Leu	atg Met 1925	cgg Arg	tct Ser	cat His	aat Asn	5820
gat Asp 1930	gag Glu	cat His	tct Ser	gat Asp	gtt Val 1935	ctt Leu	cca Pro	gtt Val	ttg Leu	gat Asp 1940	gtt Val	tgc Cys	tca Ser	ttg Leu	5865
aag Lys 1945	cat His	gtg Val	gca Ala	tat Tyr	gtt Val 1950	ttt Phe	caa Gln	gca Ala	ctt Leu	ata Ile 1955	tac Tyr	tgg Trp	att Ile	aag Lys	5910
gca Ala 1960	atg Met	aat Asn	cag Gln	cag Gln	aca Thr 1965	aca Thr	ttg Leu	gat Asp	aca Thr	cct Pro 1970	caa Gln	cta Leu	gaa Glu	cgc Arg	5955
aaa Lys 1975	agg Arg	acg Thr	cga Arg	gaa Glu	ctc Leu 1980	ttg Leu	gaa Glu	ctg Leu	ggc Gly	att Ile 1985	gat Asp	aat Asn	gaa Glu	gat Asp	6000
tca Ser 1990	gaa Glu	cat His	gaa Glu	aat Asn	gat Asp 1995	gat Asp	gac Asp	acc Thr	aat Asn	caa Gln 2000	agt Ser	gct Ala	act Thr	ttg Leu	6045
aat Asn 2005	gat Asp	aag Lys	gat Asp	gat Asp	gac Asp 2010	tct Ser	ctt Leu	cct Pro	gca Ala	gaa Glu 2015	act Thr	ggc Gly	caa Gln	aac Asn	6090
cat His 2020	cca Pro	ttt Phe	ttc Phe	cga Arg	cgt Arg 2025	tca Ser	gac Asp	tcc Ser	atg Met	aca Thr 2030	ttc Phe	ctt Leu	ggg Gly	tgt Cys	6135
ata Ile 2035	ccc Pro	cca Pro	aat Asn	cca Pro	ttt Phe 2040	gaa Glu	gtg Val	cct Pro	ctg Leu	gct Ala 2045	gaa Glu	gcc Ala	atc Ile	ccc Pro	6180

ttg gct gat cag cca cat ctg ttg cag cca aat gct aga aag gag Leu Ala Asp Gln Pro His Leu Leu Gln Pro Asn Ala Arg Lys Glu 2050 2055 2060	6225
gat ctt ttt ggc cgt cca agt cag ggt ctt tat tct tca tct gcc Asp Leu Phe Gly Arg Pro Ser Gln Gly Leu Tyr Ser Ser Ser Ala 2065 2070 2075	6270
agt agt ggg aaa tgt tta atg gag gtt aca gtg gat aga aac tgc Ser Ser Gly Lys Cys Leu Met Glu Val Thr Val Asp Arg Asn Cys 2080 2085 2090	6315
cta gag gtt ctt cca aca aaa atg tct tat gct gcc aat ctg aaa Leu Glu Val Leu Pro Thr Lys Met Ser Tyr Ala Ala Asn Leu Lys 2095 2100 2105	6360
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cag ccc gtg ctg cca gaa gaa act gag agt tca aaa cca ggg cca Gln Pro Val Leu Pro Glu Glu Thr Glu Ser Ser Lys Pro Gly Pro 2125 2130 2135	6450
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gaa ata gga ctt act gaa agt gaa ggg cca cct ctc aca tct ttc Glu Ile Gly Leu Thr Glu Ser Glu Gly Pro Pro Leu Thr Ser Phe 2155 2160 2165	6540
agg cca cag tgt agc ttt atg gga atg gtt att tcc cat gat atg Arg Pro Gln Cys Ser Phe Met Gly Met Val Ile Ser His Asp Met 2170 2175 2180	6585
ctg cta gga cgt tgg cgc ctt tct tta gaa ctg ttc ggc agg gta Leu Leu Gly Arg Trp Arg Leu Ser Leu Glu Leu Phe Gly Arg Val 2185 2190 2195	6630
ttc atg gaa gat gtt gga gca gaa cct gga tca atc cta act gaa Phe Met Glu Asp Val Gly Ala Glu Pro Gly Ser Ile Leu Thr Glu 2200 2205 2210	6675
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gaa aaa ctg aga aac cag cag tca aga gat ttg tca cta gag gtt Glu Lys Leu Arg Asn Gln Gln Ser Arg Asp Leu Ser Leu Glu Val 2230 2235 2240	6765
gat cgg gat cga gat ctt ctc att cag cag act atg agg cag ctt Asp Arg Asp Arg Asp Leu Leu Ile Gln Gln Thr Met Arg Gln Leu 2245 2250 2255	6810
aac aat cac ttt ggt cga aga tgt gct act aca cca atg gct gta Asn Asn His Phe Gly Arg Arg Cys Ala Thr Thr Pro Met Ala Val 2260 2265 2270	6855
cac aga gta aaa gtc aca ttt aag gat gag cca gga gag ggc agt His Arg Val Lys Val Thr Phe Lys Asp Glu Pro Gly Glu Gly Ser 2275 2280 2285	6900
ggt gta gca cga agt ttt tat aca gcc att gca caa gca ttt tta Gly Val Ala Arg Ser Phe Tyr Thr Ala Ile Ala Gln Ala Phe Leu 2290 2295 2300	6945



tca Ser 2305	aat gaa aaa ttg cca Asn Glu Lys Leu Pro 2310	aat cta gag tgt atc Asn Leu Glu Cys Ile 2315	caa aat gcc aac Gln Asn Ala Asn 2315	6990
aaa Lys 2320	ggc acc cac aca agt Gly Thr His Thr Ser 2325	tta atg cag aga tta Leu Met Gln Arg Leu 2330	agg aac cga gga Arg Asn Arg Gly 2330	7035
gag Glu 2335	aga gac cgg gaa agg Arg Asp Arg Glu Arg 2340	gag aga gaa agg gaa Glu Arg Glu Arg Glu 2345	atg agg agg agt Met Arg Arg Ser 2345	7080
agt Ser 2350	ggt ttg cga gca ggt Gly Leu Arg Ala Gly 2355	tct cgg agg gac cgg Ser Arg Arg Asp Arg 2360	gat aga gac ttt Asp Arg Asp Phe 2360	7125
aga Arg 2365	aga cag ctt tcc atc Arg Gln Leu Ser Ile 2370	gac act agg ccc ttt Asp Thr Arg Pro Phe 2375	aga cca gcc tct Arg Pro Ala Ser 2375	7170
gaa Glu 2380	ggg aat cct agc gat Gly Asn Pro Ser Asp 2385	gat cct gag cct ttg Asp Pro Glu Pro Leu 2390	cca gca cat cgg Pro Ala His Arg 2390	7215
cag Gln 2395	gca ctt gga gag agg Ala Leu Gly Glu Arg 2400	ctt tat cct cgt gta Leu Tyr Pro Arg Val 2405	caa gca atg caa Gln Ala Met Gln 2405	7260
cca Pro 2410	gca ttt gca agt aaa Ala Phe Ala Ser Lys 2415	atc act ggc atg ttg Ile Thr Gly Met Leu 2420	ttg gaa tta tcc Leu Glu Leu Ser 2420	7305
cca Pro 2425	gct cag ctg ctt ctc Ala Gln Leu Leu Leu 2430	ctt cta gca agt gag Leu Leu Ala Ser Glu 2435	gat tct ctg aga Asp Ser Leu Arg 2435	7350
gca Ala 2440	aga gtg gat gag gcc Arg Val Asp Glu Ala 2445	atg gaa ctc att att Met Glu Leu Ile Ile 2450	gca cat gga cgg Ala His Gly Arg 2450	7395
gaa Glu 2455	aat gga gct gat agt Asn Gly Ala Asp Ser 2460	atc ctg gat ctt gga Ile Leu Asp Leu Gly 2465	tta gta gac tcc Leu Val Asp Ser 2465	7440
tca Ser 2470	gaa aag gta cag cag Glu Lys Val Gln Gln 2475	gaa aac cga aag cgc Glu Asn Arg Lys Arg 2480	cat ggc tct agt His Gly Ser Ser 2480	7485
cga Arg 2485	agt gta gta gat atg Ser Val Val Asp Met 2490	gat tta gat gat aca Asp Leu Asp Asp Thr 2495	gat gat ggt gat Asp Asp Gly Asp 2495	7530
gac Asp 2500	aat gcc cct ttg ttt Asn Ala Pro Leu Phe 2505	tac caa cct ggg aaa Tyr Gln Pro Gly Lys 2510	aga gga ttt tat Arg Gly Phe Tyr 2510	7575
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aga Arg 2530	aac att ggc agg att Asn Ile Gly Arg Ile 2535	ctt gga cta tgt ctg Leu Gly Leu Cys Leu 2540	tta cag aat gaa Leu Gln Asn Glu 2540	7665
ctc Leu 2545	tgt cct atc aca ttg Cys Pro Ile Thr Leu 2550	aat aga cat gta att Asn Arg His Val Ile 2555	aaa gta ttg ctt Lys Val Leu Leu 2555	7710



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Lys Gln Cys Val Val Gly Pro Asn His Ala Ala Phe Leu Leu Glu Asp  
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Gly Arg Val Cys Arg Ile Gly Phe Ser Val Gln Pro Asp Arg Leu Glu  
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Gly Ala Gly Arg Thr Ser Arg Pro Gly Arg Thr Ser Asp Ser Pro Trp  
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Phe Leu Ser Gly Ser Glu Thr Leu Gly Arg Leu Ala Gly Asn Thr Leu  
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Gly Ser Arg Trp Ser Ser Gly Val Gly Gly Ser Gly Gly Gly Ser Ser  
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Gly Arg Ser Ser Ala Gly Ala Arg Asp Ser Arg Arg Gln Thr Arg Val  
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Ile Arg Thr Gly Arg Asp Arg Gly Ser Gly Leu Leu Gly Ser Gln Pro  
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Gln Pro Val Ile Pro Ala Ser Val Ile Pro Glu Glu Leu Ile Ser Gln  
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Ala Gln Val Val Leu Gln Gly Lys Ser Arg Ser Val Ile Ile Arg Glu  
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Leu Gln Arg Thr Asn Leu Asp Val Asn Leu Ala Val Asn Asn Leu Leu  
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Ser Arg Asp Asp Glu Asp Gly Asp Asp Gly Asp Asp Thr Ala Ser Glu  
225 230 235 240

Ser Tyr Leu Pro Gly Glu Asp Leu Met Ser Leu Leu Asp Ala Asp Ile  
245 250 255

His Ser Ala His Pro Ser Val Ile Ile Asp Ala Asp Ala Met Phe Ser  
260 265 270

Glu Asp Ile Ser Tyr Phe Gly Tyr Pro Ser Phe Arg Arg Ser Ser Leu  
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Ser Arg Leu Gly Ser Ser Arg Val Leu Leu Leu Pro Leu Glu Arg Asp  
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Ser Glu Leu Leu Arg Glu Arg Glu Ser Val Leu Arg Leu Arg Glu Arg  
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Arg Trp Leu Asp Gly Ala Ser Phe Asp Asn Glu Arg Gly Ser Thr Ser  
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Lys Glu Gly Glu Pro Asn Leu Asp Lys Lys Asn Thr Pro Val Gln Ser  
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Pro Val Ser Leu Gly Glu Asp Leu Gln Trp Trp Pro Asp Lys Asp Gly  
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Thr Lys Phe Ile Cys Ile Gly Ala Leu Tyr Ser Glu Leu Leu Ala Val  
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Ser Ser Lys Gly Glu Leu Tyr Gln Trp Lys Trp Ser Glu Ser Glu Pro  
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Tyr Arg Asn Ala Gln Asn Pro Ser Leu His His Pro Arg Ala Thr Phe  
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Leu Gly Leu Thr Asn Glu Lys Ile Val Leu Leu Ser Ala Asn Ser Ile  
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Arg Ala Thr Val Ala Thr Glu Asn Asn Lys Val Ala Thr Trp Val Asp  
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Glu Thr Leu Ser Ser Val Ala Ser Lys Leu Glu His Thr Ala Gln Thr  
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Tyr Ser Glu Leu Gln Gly Glu Arg Ile Val Ser Leu His Cys Cys Ala  
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Leu Tyr Thr Cys Ala Gln Leu Glu Asn Ser Leu Tyr Trp Trp Gly Val  
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Val Pro Phe Ser Gln Arg Lys Lys Met Leu Glu Lys Ala Arg Ala Lys  
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675 680 685

Thr Asn Cys Gln Asn Ser Ser Gly Pro Asp Ala Asp Pro Ser Ser Leu  
690 695 700

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Thr Gly Gly Thr Pro Lys Val Pro Asp Cys Phe Gln Arg Thr Pro Lys  
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Ser Lys Gly Val His Ala Val Leu Lys Thr Gly Asn Trp Val Arg Tyr  
755 760 765

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820 825 830

Pro Asp Trp Leu Asp Leu Pro Pro Ile Ser Ser Leu Gly Met Gly Val  
835 840 845

His Ser Leu Ile Asn Leu Pro Ala Asn Ser Thr Ile Lys Lys Lys Ala  
850 855 860

Ala Val Ile Ile Met Ala Val Glu Lys Gln Thr Leu Met Gln His Ile  
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885 890 895

Gln Ala Val Val Leu Glu Gln Asn Leu Gln Met Leu Gln Thr Phe Ile  
900 905 910

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Val Cys Phe Pro Thr Ser Asn Lys Glu Thr Lys Glu Glu Glu Ala  
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Arg Pro Pro Arg Ile Arg Glu 1295	Asp Arg Asn Arg Lys 1300	Thr Ala Ser 1305
Pro Glu Asp Ser Asp Met Pro 1310	Asp His Asp Leu Glu 1315	Pro Pro Arg 1320
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Thr His Cys Leu Ile Val Lys 1385	Cys Thr Ala Asp Ile 1390	Leu Leu Leu 1395
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Thr Pro Gly Arg Arg Glu Glu 1415	Ala Ile Ala Val Thr 1420	Met Arg Phe 1425
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Ala Ser Ser Lys Lys Lys Asn 1445	Asn Phe Ile Pro Gln 1450	Pro Ile Gly 1455
Lys Cys Lys Arg Val Phe Gln 1460	Ala Leu Leu Pro Tyr 1465	Ala Val Glu 1470
Glu Leu Cys Asn Val Ala Glu 1475	Ser Leu Ile Val Pro 1480	Val Arg Met 1485



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 1895 1900 1905  
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 1910 1915 1920  
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 1985 1990 1995

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Met 2030	Thr	Phe	Leu	Gly	Cys	Ile 2035	Pro	Pro	Asn	Pro	Phe 2040	Glu	Val	Pro
Leu 2045	Ala	Glu	Ala	Ile	Pro	Leu 2050	Ala	Asp	Gln	Pro	His 2055	Leu	Leu	Gln
Pro 2060	Asn	Ala	Arg	Lys	Glu	Asp 2065	Leu	Phe	Gly	Arg	Pro 2070	Ser	Gln	Gly
Leu 2075	Tyr	Ser	Ser	Ser	Ala	Ser 2080	Ser	Gly	Lys	Cys	Leu 2085	Met	Glu	Val
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Cys Leu Leu Gln Asn Glu Leu Cys Pro Ile Thr Leu Asn Arg His  
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Val Ile Lys Val Leu Leu Gly Arg Lys Val Asn Trp His Asp Phe  
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Cys Cys Phe Arg Asn Asn Asp His Pro Glu Ile Thr Tyr Arg Leu Arg  
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tta agg gaa cac gaa aat tca aca tta gat agg cat tta gac ttt ttt Leu Arg Glu His Glu Asn Ser Thr Leu Asp Arg His Leu Asp Phe Phe 320 325 330 335			1130
gaa atg ctc cga aat gaa gat gaa cta gaa ttt gcc aaa aga ttt gaa Glu Met Leu Arg Asn Glu Asp Glu Leu Glu Phe Ala Lys Arg Phe Glu 340 345 350			1178
ctg gtt cac ata gac aca aaa agt gca act cag atg ttt gag ctg acc Leu Val His Ile Asp Thr Lys Ser Ala Thr Gln Met Phe Glu Leu Thr 355 360 365			1226
agg aag agg ctg aca cat agt gaa gct tac ccg cat ttc atg tcc atc Arg Lys Arg Leu Thr His Ser Glu Ala Tyr Pro His Phe Met Ser Ile 370 375 380			1274
ctg cac cac tgc ctc caa atg cct tac aag agg agt ggc aac act gtt Leu His His Cys Leu Gln Met Pro Tyr Lys Arg Ser Gly Asn Thr Val			1322

385	390	395	
cag tac tgg cta cta cta gat aga att ata cag cag ata gtt atc cag Gln Tyr Trp Leu Leu Leu Asp Arg Ile Ile Gln Gln Ile Val Ile Gln 400 405 410 415			1370
aat gac aaa gga cag gac cct gac tcc aca cct ttg gaa aac ttt aat Asn Asp Lys Gly Gln Asp Pro Asp Ser Thr Pro Leu Glu Asn Phe Asn 420 425 430			1418
att aag aat gtc gta cga atg ttg gtt aat gaa aat gaa gtt aag cag Ile Lys Asn Val Val Arg Met Leu Val Asn Glu Asn Glu Val Lys Gln 435 440 445			1466
tgg aaa gaa caa gcg gaa aaa atg aga aaa gag cac aat gag cta caa Trp Lys Glu Gln Ala Glu Lys Met Arg Lys Glu His Asn Glu Leu Gln 450 455 460			1514
cag aaa ctg gaa aag aaa gaa cga gaa tgt gat gct aag act caa gag Gln Lys Leu Glu Lys Lys Glu Arg Glu Cys Asp Ala Lys Thr Gln Glu 465 470 475			1562
aag gaa gag atg atg cag acc tta aat aaa atg aaa gag aaa ctt gaa Lys Glu Glu Met Met Gln Thr Leu Asn Lys Met Lys Glu Lys Leu Glu 480 485 490 495			1610
aag gag act act gag cat aag caa gtc aag cag cag gtc gcg gac ctc Lys Glu Thr Thr Glu His Lys Gln Val Lys Gln Gln Val Ala Asp Leu 500 505 510			1658
aca gca cag ctc cat gag ctc agc agg agg gcc gtc tgt gct tca atc Thr Ala Gln Leu His Glu Leu Ser Arg Arg Ala Val Cys Ala Ser Ile 515 520 525			1706
cca ggt gga ccc tcg cct gga gca cca gga ggg ccc ttt cct tcc tct Pro Gly Gly Pro Ser Pro Gly Ala Pro Gly Gly Pro Phe Pro Ser Ser 530 535 540			1754
gtg cct gga tct ctc ctt cct ccc cca cca ccc cca cct cta cca ggt Val Pro Gly Ser Leu Leu Pro Pro Pro Pro Pro Pro Pro Leu Pro Gly 545 550 555			1802
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cct ccc cca ggg cct cct ccc tta ggg gca atc atg cca cct cct ggt Pro Pro Pro Gly Pro Pro Pro Leu Gly Ala Ile Met Pro Pro Pro Gly 580 585 590			1898
gct cca atg ggc cta gca ctg aag aag aaa agc att cct cag ccc aca Ala Pro Met Gly Leu Ala Leu Lys Lys Lys Ser Ile Pro Gln Pro Thr 595 600 605			1946
aat gcc ctg aaa tcc ttc aac tgg tct aaa ctg ccc gag aac aaa ctg Asn Ala Leu Lys Ser Phe Asn Trp Ser Lys Leu Pro Glu Asn Lys Leu 610 615 620			1994
gaa gga aca gta tgg acc gaa att gat gat aca aaa gtc ttc aaa att Glu Gly Thr Val Trp Thr Glu Ile Asp Asp Thr Lys Val Phe Lys Ile 625 630 635			2042
cta gat ctt gaa gac ctg gaa aga acc ttc tct gcc tat caa aga cag Leu Asp Leu Glu Asp Leu Glu Arg Thr Phe Ser Ala Tyr Gln Arg Gln 640 645 650 655			2090
cag gat ttc ttt gtg aac agt aac tcc aag cag aaa gaa gca gat gcc Gln Asp Phe Phe Val Asn Ser Asn Ser Lys Gln Lys Glu Ala Asp Ala 2138			



660	665	670	
att gat gac act ctg agt tcc aaa ctt aaa gtt aaa gag ctt tcg gtg Ile Asp Asp Thr Leu Ser Ser Lys Leu Lys Val Lys Glu Leu Ser Val 675 680 685			2186
att gat ggt cgg aga gct cag aat tgc aac atc ctt cta tcg agg ttg Ile Asp Gly Arg Arg Ala Gln Asn Cys Asn Ile Leu Leu Ser Arg Leu 690 695 700			2234
aaa tta tcc aat gac gaa atc aaa cgg gca att cta aca atg gac gaa Lys Leu Ser Asn Asp Glu Ile Lys Arg Ala Ile Leu Thr Met Asp Glu 705 710 715			2282
cag gaa gat ctg ccc aag gac atg ttg gaa cag ctc ttg aaa ttt gtt Gln Glu Asp Leu Pro Lys Asp Met Leu Glu Gln Leu Leu Lys Phe Val 720 725 730 735			2330
cct gaa aaa agt gac att gac cta ttg gag gaa cat aaa cac gaa ctg Pro Glu Lys Ser Asp Ile Asp Leu Leu Glu Glu His Lys His Glu Leu 740 745 750			2378
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aat cac tat cag caa agg ttg caa tcg ctg tac ttc aaa aag aag ttt Asn His Tyr Gln Gln Arg Leu Gln Ser Leu Tyr Phe Lys Lys Lys Phe 770 775 780			2474
gca gag cgt gtg gca gaa gtg aaa cct aaa gtg gaa gca att cgt tct Ala Glu Arg Val Ala Glu Val Lys Pro Lys Val Glu Ala Ile Arg Ser 785 790 795			2522
ggc tca gaa gag gtg ttt agg agt ggt gcc ctc aag cag ttg ctg gag Gly Ser Glu Glu Val Phe Arg Ser Gly Ala Leu Lys Gln Leu Leu Glu 800 805 810 815			2570
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gca tat gga ttc aag ata tct agc cta aac aaa att gct gac aca aaa Ala Tyr Gly Phe Lys Ile Ser Ser Leu Asn Lys Ile Ala Asp Thr Lys 835 840 845			2666
toc agc atc gac aaa aac att acc ctt ttg cac tat ctc atc act att Ser Ser Ile Asp Lys Asn Ile Thr Leu Leu His Tyr Leu Ile Thr Ile 850 855 860			2714
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gat att cct caa gct gcg aaa gta aac atg act gag ctg gac aaa gaa Asp Ile Pro Gln Ala Ala Lys Val Asn Met Thr Glu Leu Asp Lys Glu 880 885 890 895			2810
ata agt acc ttg aga agt ggc ttg aaa gca gta gag aca gag ctg gaa Ile Ser Thr Leu Arg Ser Gly Leu Lys Ala Val Glu Thr Glu Leu Glu 900 905 910			2858
tat cag aag tct cag ccc cca cag ccc gga gat aag ttt gtg tct gtt Tyr Gln Lys Ser Gln Pro Pro Gln Pro Gly Asp Lys Phe Val Ser Val 915 920 925			2906
gtc agc cag ttc atc aca gta gcc agc ttc agc ttc tct gat gtt gaa Val Ser Gln Phe Ile Thr Val Ala Ser Phe Ser Phe Ser Asp Val Glu 930 935 940 945			2954

930	935	940	
gac ctt cta gca gaa gct aaa gac ctg ttt act aaa gca gtg aag cac Asp Leu Leu Ala Glu Ala Lys Asp Leu Phe Thr Lys Ala Val Lys His 945 950 955			3002
ttt ggg gaa gag gct ggc aaa ata caa cca gat gag ttc ttt ggc att Phe Gly Glu Glu Ala Gly Lys Ile Gln Pro Asp Glu Phe Phe Gly Ile 960 965 970 975			3050
ttt gat caa ttt ctt caa gct gtg tca gaa gcc aaa caa gaa aac gaa Phe Asp Gln Phe Leu Gln Ala Val Ser Glu Ala Lys Gln Glu Asn Glu 980 985 990			3098
aat atg aga aag aaa aag gag gaa gaa gaa cgt cga gct cgc atg gaa Asn Met Arg Lys Lys Lys Glu Glu Glu Glu Arg Arg Ala Arg Met Glu 995 1000 1005			3146
gct cag ctc aaa gaa caa cgt gaa agg gaa cgt aaa atg aga aaa Ala Gln Leu Lys Glu Gln Arg Glu Arg Glu Arg Lys Met Arg Lys 1010 1015 1020			3191
gct aaa gag aat agt gaa gaa agc gga gag ttt gat gac ctt gtt Ala Lys Glu Asn Ser Glu Glu Ser Gly Glu Phe Asp Asp Leu Val 1025 1030 1035			3236
tca gct tta cgc tca gga gaa gtg ttt gac aaa gac ctt tct aaa Ser Ala Leu Arg Ser Gly Glu Val Phe Asp Lys Asp Leu Ser Lys 1040 1045 1050			3281
ttg aaa cgg aat cgc aaa cgt att acc aac cag atg act gac agc Leu Lys Arg Asn Arg Lys Arg Ile Thr Asn Gln Met Thr Asp Ser 1055 1060 1065			3326
agc aga gag aga cca atc aca aaa ctt aat ttc taattttcca Ser Arg Glu Arg Pro Ile Thr Lys Leu Asn Phe 1070 1075			3369
tgaatacttt tttttagaaa gctcattagc agccctctaa agtgactaga acgttttcatt			3429
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cagatttttg gaaaaaaca ctatataaat gcaatccatg ctttttttaa agaacaacat			4149
tgccagagta tgcttgttct aacaatatag atatataaac cttaaaaata ataaaatc			4209
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&lt;211&gt; 1078

&lt;212&gt; PRT

&lt;213&gt; NM\_014992 DAAM1

&lt;400&gt; 66

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Cys Phe Arg Asn Asn Asp His Pro Glu Ile Thr Tyr Arg Leu Arg Asn  
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Asp Ser Asn Phe Ala Leu Gln Thr Met Glu Pro Ala Leu Pro Met Pro  
 35 40 45

Pro Val Glu Glu Leu Asp Val Met Phe Ser Glu Leu Val Asp Glu Leu  
 50 55 60

Asp Leu Thr Asp Lys His Arg Glu Ala Met Phe Ala Leu Pro Ala Glu  
 65 70 75 80

Lys Lys Trp Gln Ile Tyr Cys Ser Lys Lys Lys Asp Gln Glu Glu Asn  
 85 90 95

Lys Gly Ala Thr Ser Trp Pro Glu Phe Tyr Ile Asp Gln Leu Asn Ser  
 100 105 110

Met Ala Ala Arg Lys Ser Leu Leu Ala Leu Glu Lys Glu Glu Glu Glu  
 115 120 125

Glu Arg Ser Lys Thr Ile Glu Ser Leu Lys Thr Ala Leu Arg Thr Lys  
 130 135 140

Pro Met Arg Phe Val Thr Arg Phe Ile Asp Leu Asp Gly Leu Ser Cys  
 145 150 155 160

Ile Leu Asn Phe Leu Lys Thr Met Asp Tyr Glu Thr Ser Glu Ser Arg  
 165 170 175

Ile His Thr Ser Leu Ile Gly Cys Ile Lys Ala Leu Met Asn Asn Ser  
 180 185 190

Gln Gly Arg Ala His Val Leu Ala His Ser Glu Ser Ile Asn Val Ile  
 195 200 205

Ala Gln Ser Leu Ser Thr Glu Asn Ile Lys Thr Lys Val Ala Val Leu  
 210 215 220

Glu Ile Leu Gly Ala Val Cys Leu Val Pro Gly Gly His Lys Lys Val  
 225 230 235 240

Leu Gln Ala Met Leu His Tyr Gln Lys Tyr Ala Ser Glu Arg Thr Arg  
 245 250 255

Phe Gln Thr Leu Ile Asn Asp Leu Asp Lys Ser Thr Gly Arg Tyr Arg  
 260 265 270

Asp Glu Val Ser Leu Lys Thr Ala Ile Met Ser Phe Ile Asn Ala Val  
 275 280 285

Leu Ser Gln Gly Ala Gly Val Glu Ser Leu Asp Phe Arg Leu His Leu  
 290 295 300

Arg Tyr Glu Phe Leu Met Leu Gly Ile Gln Pro Val Ile Asp Lys Leu  
 305 310 315 320

Arg Glu His Glu Asn Ser Thr Leu Asp Arg His Leu Asp Phe Phe Glu  
 325 330 335

Met Leu Arg Asn Glu Asp Glu Leu Glu Phe Ala Lys Arg Phe Glu Leu  
 340 345 350

Val His Ile Asp Thr Lys Ser Ala Thr Gln Met Phe Glu Leu Thr Arg  
 355 360 365

Lys Arg Leu Thr His Ser Glu Ala Tyr Pro His Phe Met Ser Ile Leu  
 370 375 380

His His Cys Leu Gln Met Pro Tyr Lys Arg Ser Gly Asn Thr Val Gln  
 385 390 395 400

Tyr Trp Leu Leu Leu Asp Arg Ile Ile Gln Gln Ile Val Ile Gln Asn  
 405 410 415

Asp Lys Gly Gln Asp Pro Asp Ser Thr Pro Leu Glu Asn Phe Asn Ile  
 420 425 430

Lys Asn Val Val Arg Met Leu Val Asn Glu Asn Glu Val Lys Gln Trp  
 435 440 445

Lys Glu Gln Ala Glu Lys Met Arg Lys Glu His Asn Glu Leu Gln Gln  
 450 455 460

Lys Leu Glu Lys Lys Glu Arg Glu Cys Asp Ala Lys Thr Gln Glu Lys  
 465 470 475 480

Glu Glu Met Met Gln Thr Leu Asn Lys Met Lys Glu Lys Leu Glu Lys  
 485 490 495

Glu Thr Thr Glu His Lys Gln Val Lys Gln Gln Val Ala Asp Leu Thr  
500 505 510

Ala Gln Leu His Glu Leu Ser Arg Arg Ala Val Cys Ala Ser Ile Pro  
515 520 525

Gly Gly Pro Ser Pro Gly Ala Pro Gly Gly Pro Phe Pro Ser Ser Val  
530 535 540

Pro Gly Ser Leu Leu Pro Pro Pro Pro Pro Pro Pro Leu Pro Gly Gly  
545 550 555 560

Met Leu Pro Pro Pro Pro Pro Pro Leu Pro Pro Gly Gly Pro Pro Pro  
565 570 575

Pro Pro Gly Pro Pro Pro Leu Gly Ala Ile Met Pro Pro Pro Gly Ala  
580 585 590

Pro Met Gly Leu Ala Leu Lys Lys Lys Ser Ile Pro Gln Pro Thr Asn  
595 600 605

Ala Leu Lys Ser Phe Asn Trp Ser Lys Leu Pro Glu Asn Lys Leu Glu  
610 615 620

Gly Thr Val Trp Thr Glu Ile Asp Asp Thr Lys Val Phe Lys Ile Leu  
625 630 635 640

Asp Leu Glu Asp Leu Glu Arg Thr Phe Ser Ala Tyr Gln Arg Gln Gln  
645 650 655

Asp Phe Phe Val Asn Ser Asn Ser Lys Gln Lys Glu Ala Asp Ala Ile  
660 665 670

Asp Asp Thr Leu Ser Ser Lys Leu Lys Val Lys Glu Leu Ser Val Ile  
675 680 685

Asp Gly Arg Arg Ala Gln Asn Cys Asn Ile Leu Leu Ser Arg Leu Lys  
690 695 700

Leu Ser Asn Asp Glu Ile Lys Arg Ala Ile Leu Thr Met Asp Glu Gln  
705 710 715 720

Glu Asp Leu Pro Lys Asp Met Leu Glu Gln Leu Leu Lys Phe Val Pro  
725 730 735

Glu Lys Ser Asp Ile Asp Leu Leu Glu Glu His Lys His Glu Leu Asp  
740 745 750

Arg Met Ala Lys Ala Asp Arg Phe Leu Phe Glu Met Ser Arg Ile Asn

755	760	765
His Tyr Gln Gln Arg Leu Gln Ser Leu Tyr Phe Lys Lys Lys Phe Ala 770 775 780		
Glu Arg Val Ala Glu Val Lys Pro Lys Val Glu Ala Ile Arg Ser Gly 785 790 795 800		
Ser Glu Glu Val Phe Arg Ser Gly Ala Leu Lys Gln Leu Leu Glu Val 805 810 815		
Val Leu Ala Phe Gly Asn Tyr Met Asn Lys Gly Gln Arg Gly Asn Ala 820 825 830		
Tyr Gly Phe Lys Ile Ser Ser Leu Asn Lys Ile Ala Asp Thr Lys Ser 835 840 845		
Ser Ile Asp Lys Asn Ile Thr Leu Leu His Tyr Leu Ile Thr Ile Val 850 855 860		
Glu Asn Lys Tyr Pro Ser Val Leu Asn Leu Asn Glu Glu Leu Arg Asp 865 870 875 880		
Ile Pro Gln Ala Ala Lys Val Asn Met Thr Glu Leu Asp Lys Glu Ile 885 890 895		
Ser Thr Leu Arg Ser Gly Leu Lys Ala Val Glu Thr Glu Leu Glu Tyr 900 905 910		
Gln Lys Ser Gln Pro Pro Gln Pro Gly Asp Lys Phe Val Ser Val Val 915 920 925		
Ser Gln Phe Ile Thr Val Ala Ser Phe Ser Phe Ser Asp Val Glu Asp 930 935 940		
Leu Leu Ala Glu Ala Lys Asp Leu Phe Thr Lys Ala Val Lys His Phe 945 950 955 960		
Gly Glu Glu Ala Gly Lys Ile Gln Pro Asp Glu Phe Phe Gly Ile Phe 965 970 975		
Asp Gln Phe Leu Gln Ala Val Ser Glu Ala Lys Gln Glu Asn Glu Asn 980 985 990		
Met Arg Lys Lys Lys Glu Glu Glu Glu Arg Arg Ala Arg Met Glu Ala 995 1000 1005		
Gln Leu Lys Glu Gln Arg Glu Arg Glu Arg Lys Met Arg Lys Ala 1010 1015 1020		
Lys Glu Asn Ser Glu Glu Ser Gly Glu Phe Asp Asp Leu Val Ser		

1025                      1030                      1035

Ala Leu Arg Ser Gly Glu Val Phe Asp Lys Asp Leu Ser Lys Leu  
 1040                      1045                      1050

Lys Arg Asn Arg Lys Arg Ile Thr Asn Gln Met Thr Asp Ser Ser  
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Arg Glu Arg Pro Ile Thr Lys Leu Asn Phe  
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<211> 1096

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<222> (1)..(765)

<223>

<400> 67

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 Met Ile Leu Asn Lys Ala Leu Leu Leu Gly Ala Leu Ala Leu Thr Thr  
 1                      5                      10                      15

gtg atg agc ccc tgt gga ggt gaa gac att gtg gct gac cac gtt gcc 96  
 Val Met Ser Pro Cys Gly Gly Glu Asp Ile Val Ala Asp His Val Ala  
                     20                      25                      30

tct tgt ggt gta aac ttg tac cag ttt tac ggt ccc tct ggc cag tac 144  
 Ser Cys Gly Val Asn Leu Tyr Gln Phe Tyr Gly Pro Ser Gly Gln Tyr  
                     35                      40                      45

acc cat gaa ttt gat gga gat gag cag ttc tac gtg gac ctg gag agg 192  
 Thr His Glu Phe Asp Gly Asp Glu Gln Phe Tyr Val Asp Leu Glu Arg  
                     50                      55                      60

aag gag act gcc tgg cgg tgg cct gag ttc agc aaa ttt gga ggt ttt 240  
 Lys Glu Thr Ala Trp Arg Trp Pro Glu Phe Ser Lys Phe Gly Gly Phe  
 65                      70                      75                      80

gac ccg cag ggt gca ctg aga aac atg gct gtg gca aaa cac aac ttg 288  
 Asp Pro Gln Gly Ala Leu Arg Asn Met Ala Val Ala Lys His Asn Leu  
                     85                      90                      95

aac atc atg att aaa cgc tac aac tct acc gct gct acc aat gag gtt 336  
 Asn Ile Met Ile Lys Arg Tyr Asn Ser Thr Ala Ala Thr Asn Glu Val  
                     100                      105                      110

cct gag gtc aca gtg ttt tcc aag tct ccc gtg aca ctg ggt cag ccc 384  
 Pro Glu Val Thr Val Phe Ser Lys Ser Pro Val Thr Leu Gly Gln Pro  
                     115                      120                      125

aac acc ctc att tgt ctt gtg gac aac atc ttt cct cct gtg gtc aac 432  
 Asn Thr Leu Ile Cys Leu Val Asp Asn Ile Phe Pro Pro Val Val Asn  
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 Ile Thr Trp Leu Ser Asn Gly Gln Ser Val Thr Glu Gly Val Ser Glu  
 145 150 155 160  
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 Thr Ser Phe Leu Ser Lys Ser Asp His Ser Phe Phe Lys Ile Ser Tyr  
 165 170 175  
 ctc acc ttc ctc cct tct gct gat gag att tat gac tgc aag gtg gag 576  
 Leu Thr Phe Leu Pro Ser Ala Asp Glu Ile Tyr Asp Cys Lys Val Glu  
 180 185 190  
 cac tgg ggc ctg gac cag cct ctt ctg aaa cac tgg gag cct gag att 624  
 His Trp Gly Leu Asp Gln Pro Leu Leu Lys His Trp Glu Pro Glu Ile  
 195 200 205  
 cca gcc cct atg tca gag ctc aca gag act gtg gtc tgt gcc ctg ggg 672  
 Pro Ala Pro Met Ser Glu Leu Thr Glu Thr Val Val Cys Ala Leu Gly  
 210 215 220  
 ttg tct gtg ggc ctc atg ggc att gtg gtg ggc act gtc ttc atc atc 720  
 Leu Ser Val Gly Leu Met Gly Ile Val Val Gly Thr Val Phe Ile Ile  
 225 230 235 240  
 caa ggc ctg cgt tca gtt ggt gct tcc aga cac caa ggg cca ttg 765  
 Gln Gly Leu Arg Ser Val Gly Ala Ser Arg His Gln Gly Pro Leu  
 245 250 255  
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 ctaaatagacc tagcactatt ctctggcccc atttatcata tcccttttct cctccaaata 885  
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&lt;210&gt; 68

&lt;211&gt; 255

&lt;212&gt; PRT

&lt;213&gt; NM\_002122 MHC class II DQ alpha 1, HLA-DQA1

&lt;400&gt; 68

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 20 25 30

Ser Cys Gly Val Asn Leu Tyr Gln Phe Tyr Gly Pro Ser Gly Gln Tyr  
 35 40 45



Thr His Glu Phe Asp Gly Asp Glu Gln Phe Tyr Val Asp Leu Glu Arg  
 50 55 60

Lys Glu Thr Ala Trp Arg Trp Pro Glu Phe Ser Lys Phe Gly Gly Phe  
 65 70 75 80

Asp Pro Gln Gly Ala Leu Arg Asn Met Ala Val Ala Lys His Asn Leu  
 85 90 95

Asn Ile Met Ile Lys Arg Tyr Asn Ser Thr Ala Ala Thr Asn Glu Val  
 100 105 110

Pro Glu Val Thr Val Phe Ser Lys Ser Pro Val Thr Leu Gly Gln Pro  
 115 120 125

Asn Thr Leu Ile Cys Leu Val Asp Asn Ile Phe Pro Pro Val Val Asn  
 130 135 140

Ile Thr Trp Leu Ser Asn Gly Gln Ser Val Thr Glu Gly Val Ser Glu  
 145 150 155 160

Thr Ser Phe Leu Ser Lys Ser Asp His Ser Phe Phe Lys Ile Ser Tyr  
 165 170 175

Leu Thr Phe Leu Pro Ser Ala Asp Glu Ile Tyr Asp Cys Lys Val Glu  
 180 185 190

His Trp Gly Leu Asp Gln Pro Leu Leu Lys His Trp Glu Pro Glu Ile  
 195 200 205

Pro Ala Pro Met Ser Glu Leu Thr Glu Thr Val Val Cys Ala Leu Gly  
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Leu Ser Val Gly Leu Met Gly Ile Val Val Gly Thr Val Phe Ile Ile  
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<210> 69

<211> 2820

<212> DNA

<213> NM\_003014 SFRP4, secreted frizzled-related protein 4

<220>

<221> CDS

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&lt;223&gt;

&lt;400&gt; 69

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aaactctcct gcgccccaga agatttcttc ctgcggcgaag ggacagcgaa agatgagggt      180
ggcaggaaga gaaggcgctt tctgtctgcc ggggtcgcag cgcgagaggg cagtgcc          237
atg ttc ctc tcc atc cta gtg gcg ctg tgc ctg tgg ctg cac ctg gcg          285
Met Phe Leu Ser Ile Leu Val Ala Leu Cys Leu Trp Leu His Leu Ala
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Leu Gly Val Arg Gly Ala Pro Cys Glu Ala Val Arg Ile Pro Met Cys
20      25      30
cgg cac atg ccc tgg aac atc acg cgg atg ccc aac cac ctg cac cac          381
Arg His Met Pro Trp Asn Ile Thr Arg Met Pro Asn His Leu His His
35      40      45
agc acg cag gag aac gcc atc ctg gcc atc gag cag tac gag gag ctg          429
Ser Thr Gln Glu Asn Ala Ile Leu Ala Ile Glu Gln Tyr Glu Glu Leu
50      55      60
gtg gac gtg aac tgc agc gcc gtg ctg cgc ttc ttc ttc tgt gcc atg          477
Val Asp Val Asn Cys Ser Ala Val Leu Arg Phe Phe Phe Cys Ala Met
65      70      75      80
tac gcg ccc att tgc acc ctg gag ttc ctg cac gac cct atc aag ccg          525
Tyr Ala Pro Ile Cys Thr Leu Glu Phe Leu His Asp Pro Ile Lys Pro
85      90      95
tgc aag tcg gtg tgc caa cgc gcg cgc gac gac tgc gag ccc ctc atg          573
Cys Lys Ser Val Cys Gln Arg Ala Arg Asp Asp Cys Glu Pro Leu Met
100      105      110
aag atg tac aac cac agc tgg ccc gaa agc ctg gcc tgc gac gag ctg          621
Lys Met Tyr Asn His Ser Trp Pro Glu Ser Leu Ala Cys Asp Glu Leu
115      120      125
cct gtc tat gac cgt ggc gtg tgc att tcg cct gaa gcc atc gtc acg          669
Pro Val Tyr Asp Arg Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr
130      135      140
gac ctc ccg gag gat gtt aag tgg ata gac atc aca cca gac atg atg          717
Asp Leu Pro Glu Asp Val Lys Trp Ile Asp Ile Thr Pro Asp Met Met
145      150      155      160
gta cag gaa agg cct ctt gat gtt gac tgt aaa cgc cta agc ccc gat          765
Val Gln Glu Arg Pro Leu Asp Val Asp Cys Lys Arg Leu Ser Pro Asp
165      170      175
cgg tgc aag tgt aaa aag gtg aag cca act ttg gca acg tat ctc agc          813
Arg Cys Lys Cys Lys Lys Val Lys Pro Thr Leu Ala Thr Tyr Leu Ser
180      185      190
aaa aac tac agc tat gtt att cat gcc aaa ata aaa gct gtg cag agg          861
Lys Asn Tyr Ser Tyr Val Ile His Ala Lys Ile Lys Ala Val Gln Arg
195      200      205
agt ggc tgc aat gag gtc aca acg gtg gtg gat gta aaa gag atc ttc          909

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[illegible]

gacagttggg atactttaat cagaaaaaaa gaacttattt gcagcatttt atcaacaaat 2375  
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 taacacagta agcatgtatt ttataaggca ttcaataaat gcacaacgcc caaaggaaat 2495  
 aaaatcctat ctaatcctac tctccactac acagaggtaa tcactattag tattttggca 2555  
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 aacctgtata catgtgtttc ataacctgcc tcctttgctt ggccttttat tgagataagt 2675  
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<210> 70

<211> 346

<212> PRT

<213> NM\_003014 SFRP4, secreted frizzled-related protein 4

<400> 70

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 20 25 30

Arg His Met Pro Trp Asn Ile Thr Arg Met Pro Asn His Leu His His  
 35 40 45

Ser Thr Gln Glu Asn Ala Ile Leu Ala Ile Glu Gln Tyr Glu Glu Leu  
 50 55 60

Val Asp Val Asn Cys Ser Ala Val Leu Arg Phe Phe Phe Cys Ala Met  
 65 70 75 80

Tyr Ala Pro Ile Cys Thr Leu Glu Phe Leu His Asp Pro Ile Lys Pro  
 85 90 95

Cys Lys Ser Val Cys Gln Arg Ala Arg Asp Asp Cys Glu Pro Leu Met  
 100 105 110

Lys Met Tyr Asn His Ser Trp Pro Glu Ser Leu Ala Cys Asp Glu Leu  
 115 120 125

Pro Val Tyr Asp Arg Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr  
 130 135 140

Asp Leu Pro Glu Asp Val Lys Trp Ile Asp Ile Thr Pro Asp Met Met  
 145 150 155 160

Val Gln Glu Arg Pro Leu Asp Val Asp Cys Lys Arg Leu Ser Pro Asp  
 165 170 175

Arg Cys Lys Cys Lys Lys Val Lys Pro Thr Leu Ala Thr Tyr Leu Ser  
 180 185 190

Lys Asn Tyr Ser Tyr Val Ile His Ala Lys Ile Lys Ala Val Gln Arg  
 195 200 205

Ser Gly Cys Asn Glu Val Thr Thr Val Val Asp Val Lys Glu Ile Phe  
 210 215 220

Lys Ser Ser Ser Pro Ile Pro Arg Thr Gln Val Pro Leu Ile Thr Asn  
 225 230 235 240

Ser Ser Cys Gln Cys Pro His Ile Leu Pro His Gln Asp Val Leu Ile  
 245 250 255

Met Cys Tyr Glu Trp Arg Ser Arg Met Met Leu Leu Glu Asn Cys Leu  
 260 265 270

Val Glu Lys Trp Arg Asp Gln Leu Ser Lys Arg Ser Ile Gln Trp Glu  
 275 280 285

Glu Arg Leu Gln Glu Gln Arg Arg Thr Val Gln Asp Lys Lys Lys Thr  
 290 295 300

Ala Gly Arg Thr Ser Arg Ser Asn Pro Pro Lys Pro Lys Gly Lys Pro  
 305 310 315 320

Pro Ala Pro Lys Pro Ala Ser Pro Lys Lys Asn Ile Lys Thr Arg Ser  
 325 330 335

Ala Gln Lys Arg Thr Asn Pro Lys Arg Val  
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<210> 71

<211> 1362

<212> DNA

<213> NM\_004039 annexin A2

<220>

<221> CDS

<222> (50)..(1066)

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Val	His	Glu	Ile	Leu	Cys	Lys	Leu	Ser	Leu	Glu	Gly	Asp	His	Ser	Thr	
5 10 15																
ccc	cca	agt	gca	tat	ggg	tct	gtc	aaa	gcc	tat	act	aac	ttt	gat	gct	154
Pro	Pro	Ser	Ala	Tyr	Gly	Ser	Val	Lys	Ala	Tyr	Thr	Asn	Phe	Asp	Ala	
20 25 30 35																
gag	cgg	gat	gct	ttg	aac	att	gaa	aca	gcc	atc	aag	acc	aaa	ggg	gtg	202
Glu	Arg	Asp	Ala	Leu	Asn	Ile	Glu	Thr	Ala	Ile	Lys	Thr	Lys	Gly	Val	
40 45 50																
gat	gag	gtc	acc	att	gtc	aac	att	ttg	acc	aac	cgc	agc	aat	gca	cag	250
Asp	Glu	Val	Thr	Ile	Val	Asn	Ile	Leu	Thr	Asn	Arg	Ser	Asn	Ala	Gln	
55 60 65																
aga	cag	gat	att	gcc	ttc	gcc	tac	cag	aga	agg	acc	aaa	aag	gaa	ctt	298
Arg	Gln	Asp	Ile	Ala	Phe	Ala	Tyr	Gln	Arg	Arg	Thr	Lys	Lys	Glu	Leu	
70 75 80																
gca	tea	gca	ctg	aag	tca	gcc	tta	tct	ggo	cac	ctg	gag	acg	gtg	att	346
Ala	Ser	Ala	Leu	Lys	Ser	Ala	Leu	Ser	Gly	His	Leu	Glu	Thr	Val	Ile	
85 90 95																
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Leu	Gly	Leu	Leu	Lys	Thr	Pro	Ala	Gln	Tyr	Asp	Ala	Ser	Glu	Leu	Lys	
100 105 110 115																
gct	tcc	atg	aag	ggg	ctg	gga	acc	gac	gag	gac	tct	ctc	att	gag	atc	442
Ala	Ser	Met	Lys	Gly	Leu	Gly	Thr	Asp	Glu	Asp	Ser	Leu	Ile	Glu	Ile	
120 125 130																
atc	tgc	tcc	aga	acc	aac	cag	gag	ctg	cag	gaa	att	aac	aga	gtc	tac	490
Ile	Cys	Ser	Arg	Thr	Asn	Gln	Glu	Leu	Gln	Glu	Ile	Asn	Arg	Val	Tyr	
135 140 145																
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Lys	Glu	Met	Tyr	Lys	Thr	Asp	Leu	Glu	Lys	Asp	Ile	Ile	Ser	Asp	Thr	
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tct	ggg	gac	ttc	cgc	aag	ctg	atg	gtt	gcc	ctg	gca	aag	ggg	aga	aga	586
Ser	Gly	Asp	Phe	Arg	Lys	Leu	Met	Val	Ala	Leu	Ala	Lys	Gly	Arg	Arg	
165 170 175																
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Ala	Glu	Asp	Gly	Ser	Val	Ile	Asp	Tyr	Glu	Leu	Ile	Asp	Gln	Asp	Ala	
180 185 190 195																
cgg	gat	ctc	tat	gac	gct	gga	gtg	aag	agg	aaa	gga	act	gat	gtt	ccc	682
Arg	Asp	Leu	Tyr	Asp	Ala	Gly	Val	Lys	Arg	Lys	Gly	Thr	Asp	Val	Pro	
200 205 210																
aag	tgg	atc	agc	atc	atg	acc	gag	cgg	agc	gtg	ccc	cac	ctc	cag	aaa	730
Lys	Trp	Ile	Ser	Ile	Met	Thr	Glu	Arg	Ser	Val	Pro	His	Leu	Gln	Lys	
215 220 225																
gta	ttt	gat	agg	tac	aag	agt	tac	agc	cct	tat	gac	atg	ttg	gaa	agc	778
Val	Phe	Asp	Arg	Tyr	Lys	Ser	Tyr	Ser	Pro	Tyr	Asp	Met	Leu	Glu	Ser	
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 Ile Arg Lys Glu Val Lys Gly Asp Leu Glu Asn Ala Phe Leu Asn Leu  
 245 250 255

gtt cag tgc att cag aac aag ccc ctg tat ttt gct gat cgg ctg tat 874  
 Val Gln Cys Ile Gln Asn Lys Pro Leu Tyr Phe Ala Asp Arg Leu Tyr  
 260 265 270 275

gac tcc atg aag ggc aag ggg acg cga gat aag gtc ctg atc aga atc 922  
 Asp Ser Met Lys Gly Lys Gly Thr Arg Asp Lys Val Leu Ile Arg Ile  
 280 285 290

atg gtc tcc cgc agt gaa gtg gac atg ttg aaa att agg tct gaa ttc 970  
 Met Val Ser Arg Ser Glu Val Asp Met Leu Lys Ile Arg Ser Glu Phe  
 295 300 305

aag aga aag tac ggc aag tcc ctg tac tat tat atc cag caa gac act 1018  
 Lys Arg Lys Tyr Gly Lys Ser Leu Tyr Tyr Tyr Ile Gln Gln Asp Thr  
 310 315 320

aag ggc gac tac cag aaa gcg ctg ctg tac ctg tgt ggt gga gat gac 1066  
 Lys Gly Asp Tyr Gln Lys Ala Leu Leu Tyr Leu Cys Gly Gly Asp Asp  
 325 330 335

tgaagcccgga cacggcctga gcgtccagaa atgggtgctca ccatgcttcc agctaacagg 1126

tctagaaaac cagcttgcca ataacagtcc ccgtggccat ccctgtgagg gtgacgttag 1186

cattaccccc aacctcattt tagttgccta agcattgcct ggccttctctg tctagtctct 1246

cctgtaagcc aaagaaatga acattccaag gagttggaag tgaagtctat gatgtgaaac 1306

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<210> 72

<211> 339

<212> PRT

<213> NM\_004039 annexin A2

<400> 72

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His Ser Thr Pro Pro Ser Ala Tyr Gly Ser Val Lys Ala Tyr Thr Asn  
 20 25 30

Phe Asp Ala Glu Arg Asp Ala Leu Asn Ile Glu Thr Ala Ile Lys Thr  
 35 40 45

Lys Gly Val Asp Glu Val Thr Ile Val Asn Ile Leu Thr Asn Arg Ser  
 50 55 60

Asn Ala Gln Arg Gln Asp Ile Ala Phe Ala Tyr Gln Arg Arg Thr Lys  
 65 70 75 80

Lys Glu Leu Ala Ser Ala Leu Lys Ser Ala Leu Ser Gly His Leu Glu  
85 90 95

Thr Val Ile Leu Gly Leu Leu Lys Thr Pro Ala Gln Tyr Asp Ala Ser  
100 105 110

Glu Leu Lys Ala Ser Met Lys Gly Leu Gly Thr Asp Glu Asp Ser Leu  
115 120 125

Ile Glu Ile Ile Cys Ser Arg Thr Asn Gln Glu Leu Gln Glu Ile Asn  
130 135 140

Arg Val Tyr Lys Glu Met Tyr Lys Thr Asp Leu Glu Lys Asp Ile Ile  
145 150 155 160

Ser Asp Thr Ser Gly Asp Phe Arg Lys Leu Met Val Ala Leu Ala Lys  
165 170 175

Gly Arg Arg Ala Glu Asp Gly Ser Val Ile Asp Tyr Glu Leu Ile Asp  
180 185 190

Gln Asp Ala Arg Asp Leu Tyr Asp Ala Gly Val Lys Arg Lys Gly Thr  
195 200 205

Asp Val Pro Lys Trp Ile Ser Ile Met Thr Glu Arg Ser Val Pro His  
210 215 220

Leu Gln Lys Val Phe Asp Arg Tyr Lys Ser Tyr Ser Pro Tyr Asp Met  
225 230 235 240

Leu Glu Ser Ile Arg Lys Glu Val Lys Gly Asp Leu Glu Asn Ala Phe  
245 250 255

Leu Asn Leu Val Gln Cys Ile Gln Asn Lys Pro Leu Tyr Phe Ala Asp  
260 265 270

Arg Leu Tyr Asp Ser Met Lys Gly Lys Gly Thr Arg Asp Lys Val Leu  
275 280 285

Ile Arg Ile Met Val Ser Arg Ser Glu Val Asp Met Leu Lys Ile Arg  
290 295 300

Ser Glu Phe Lys Arg Lys Tyr Gly Lys Ser Leu Tyr Tyr Tyr Ile Gln  
305 310 315 320

Gln Asp Thr Lys Gly Asp Tyr Gln Lys Ala Leu Leu Tyr Leu Cys Gly  
325 330 335

Gly Asp Asp



&lt;210&gt; 73

&lt;211&gt; 850

&lt;212&gt; DNA

&lt;213&gt; NM\_003955 SOCS3

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (107)..(781)

&lt;223&gt;

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 Met Val Thr  
 1  
 cac agc aag ttt ccc gcc gcc ggg atg agc cgc ccc ctg gac acc agc 163  
 His Ser Lys Phe Pro Ala Ala Gly Met Ser Arg Pro Leu Asp Thr Ser  
 5 10 15  
 ctg cgc ctc aag acc ttc agc tcc aag agc gag tac cag ctg gtg gtg 211  
 Leu Arg Leu Lys Thr Phe Ser Ser Lys Ser Glu Tyr Gln Leu Val Val  
 20 25 30 35  
 aac gca gtg cgc aag ctg cag gag agc ggc ttc tac tgg agc gca gtg 259  
 Asn Ala Val Arg Lys Leu Gln Glu Ser Gly Phe Tyr Trp Ser Ala Val  
 40 45 50  
 acc ggc ggc gag gcg aac ctg ctg ctc agt gcc gag ccc gcc ggc acc 307  
 Thr Gly Gly Glu Ala Asn Leu Leu Leu Ser Ala Glu Pro Ala Gly Thr  
 55 60 65  
 ttt ctg atc cgc gac agc tcg gac cag cgc cac ttc ttc acg ctc agc 355  
 Phe Leu Ile Arg Asp Ser Ser Asp Gln Arg His Phe Phe Thr Leu Ser  
 70 75 80  
 gtc aag acc cag tct ggg acc aag aac ctg cgc atc cag tgt gag ggg 403  
 Val Lys Thr Gln Ser Gly Thr Lys Asn Leu Arg Ile Gln Cys Glu Gly  
 85 90 95  
 ggc agc ttc tct ctg cag agc gat ccc cgg agc acg cag ccc gtg ccc 451  
 Gly Ser Phe Ser Leu Gln Ser Asp Pro Arg Ser Thr Gln Pro Val Pro  
 100 105 110 115  
 cgc ttc gac tgc gtg ctc aag ctg gtg tac cac tac atg ccg ccc cct 499  
 Arg Phe Asp Cys Val Leu Lys Leu Val Tyr His Tyr Met Pro Pro Pro  
 120 125 130  
 gga gcc ccc tcc ttc ccc tcg cca cct act gaa ccc tcc tcc gag gtg 547  
 Gly Ala Pro Ser Phe Pro Ser Pro Pro Thr Glu Pro Ser Ser Glu Val  
 135 140 145  
 ccc gag cag ccg tct gcc cag cca ctc cct ggg agt ccc ccc aga aga 595  
 Pro Glu Gln Pro Ser Ala Gln Pro Leu Pro Gly Ser Pro Pro Arg Arg  
 150 155 160  
 gcc tat tac atc tac tcc ggg ggc gag aag atc ccc ctg gtg ttg agc 643

Ala Tyr Tyr Ile Tyr Ser Gly Gly Glu Lys Ile Pro Leu Val Leu Ser  
 165 170 175

cgg ccc ctc tcc tcc aac gtg gcc act ctt cag cat ctc tgt cgg aag 691  
 Arg Pro Leu Ser Ser Asn Val Ala Thr Leu Gln His Leu Cys Arg Lys  
 180 185 190 195

acc gtc aac ggc cac ctg gac tcc tat gag aaa gtc acc cag ctg ccg 739  
 Thr Val Asn Gly His Leu Asp Ser Tyr Glu Lys Val Thr Gln Leu Pro  
 200 205 210

ggg ccc att cgg gag ttc ctg gac cag tac gat gcc ccg ctt 781  
 Gly Pro Ile Arg Glu Phe Leu Asp Gln Tyr Asp Ala Pro Leu  
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<210> 74

<211> 225

<212> PRT

<213> NM\_003955 SOCS3

<400> 74

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 20 25 30

Leu Val Val Asn Ala Val Arg Lys Leu Gln Glu Ser Gly Phe Tyr Trp  
 35 40 45

Ser Ala Val Thr Gly Gly Glu Ala Asn Leu Leu Leu Ser Ala Glu Pro  
 50 55 60

Ala Gly Thr Phe Leu Ile Arg Asp Ser Ser Asp Gln Arg His Phe Phe  
 65 70 75 80

Thr Leu Ser Val Lys Thr Gln Ser Gly Thr Lys Asn Leu Arg Ile Gln  
 85 90 95

Cys Glu Gly Gly Ser Phe Ser Leu Gln Ser Asp Pro Arg Ser Thr Gln  
 100 105 110

Pro Val Pro Arg Phe Asp Cys Val Leu Lys Leu Val Tyr His Tyr Met  
 115 120 125

Pro Pro Pro Gly Ala Pro Ser Phe Pro Ser Pro Pro Thr Glu Pro Ser  
 130 135 140

Ser Glu Val Pro Glu Gln Pro Ser Ala Gln Pro Leu Pro Gly Ser Pro  
145 150 155 160

Pro Arg Arg Ala Tyr Tyr Ile Tyr Ser Gly Gly Glu Lys Ile Pro Leu  
165 170 175

Val Leu Ser Arg Pro Leu Ser Ser Asn Val Ala Thr Leu Gln His Leu  
180 185 190

Cys Arg Lys Thr Val Asn Gly His Leu Asp Ser Tyr Glu Lys Val Thr  
195 200 205

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210 215 220

Leu  
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<210> 75

<211> 369

<212> DNA

<213> NM\_000331. SAA1, serum amyloid A1

<220>

<221> CDS

<222> (1)..(366)

<223>

<400> 75

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1 5 10 15

agc agc cga agc ttc ttt tgc ttc ctt ggc gag gct ttt gat ggg gct 96  
Ser Ser Arg Ser Phe Phe Ser Phe Leu Gly Glu Ala Phe Asp Gly Ala  
20 25 30

cgg gac atg tgg aga gcc tac tct gac atg aga gaa gcc aat tac atc 144  
Arg Asp Met Trp Arg Ala Tyr Ser Asp Met Arg Glu Ala Asn Tyr Ile  
35 40 45

ggc tca gac aaa tac ttc cat gct cgg ggg aac tat gat gct gcc aaa 192  
Gly Ser Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Lys  
50 55 60

agg gga cct ggg ggt gtc tgg gct gca gaa gcg atc agc gat gcc aga 240  
Arg Gly Pro Gly Gly Val Trp Ala Ala Glu Ala Ile Ser Asp Ala Arg  
65 70 75 80

gag aat atc cag aga ttc ttt ggc cat ggt gcg gag gac tgc ctg gct 288  
Glu Asn Ile Gln Arg Phe Phe Gly His Gly Ala Glu Asp Ser Leu Ala  
85 90 95

gat cag gct gcc aat gaa tgg ggc agg agt ggc aaa gac ccc aat cac 336  
 Asp Gln Ala Ala Asn Glu Trp Gly Arg Ser Gly Lys Asp Pro Asn His  
           100                          105                          110

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 Phe Arg Pro Ala Gly Leu Pro Glu Lys Tyr  
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<210> 76

<211> 122

<212> PRT

<213> NM\_000331 SAA1, serum amyloid A1

<400> 76

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           20                          25                          30

Arg Asp Met Trp Arg Ala Tyr Ser Asp Met Arg Glu Ala Asn Tyr Ile  
           35                          40                          45

Gly Ser Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Lys  
           50                          55                          60

Arg Gly Pro Gly Gly Val Trp Ala Ala Glu Ala Ile Ser Asp Ala Arg  
           65                          70                          75                          80

Glu Asn Ile Gln Arg Phe Phe Gly His Gly Ala Glu Asp Ser Leu Ala  
           85                          90                          95

Asp Gln Ala Ala Asn Glu Trp Gly Arg Ser Gly Lys Asp Pro Asn His  
           100                          105                          110

Phe Arg Pro Ala Gly Leu Pro Glu Lys Tyr  
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<210> 77

<211> 895

<212> DNA

<213> NM\_014059 RGC32

<220>

<221> CDS

&lt;222&gt; (147)..(497)

&lt;223&gt;

&lt;400&gt; 77

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gtgcggggaca gcaagccccc gaatagcccc ggctgccacc tcgcaggacc caaggccacg 120

cgcgccgggc ccagctgagc cgcctc atg aag ccg ccc gcg gag gac ctg tcg 173  
Met Lys Pro Pro Ala Glu Asp Leu Ser  
1 5

gac gcg ctg tgc gag ttt gac gcg gtg ctg gcc gac ttc gcg tcg ccc 221  
Asp Ala Leu Cys Glu Phe Asp Ala Val Leu Ala Asp Phe Ala Ser Pro  
10 15 20 25

ttc cac gag cgc cac ttc cac tac gag gag cac ctg gag cgc atg aag 269  
Phe His Glu Arg His Phe His Tyr Glu Glu His Leu Glu Arg Met Lys  
30 35 40

cgg cgc agc agc gcc agt gtc agc gac agc agc ggc ttc agc gac tcg 317  
Arg Arg Ser Ser Ala Ser Val Ser Asp Ser Ser Gly Phe Ser Asp Ser  
45 50 55

gag agt gca gat tca ctt tat agg aac agc ttc agc ttc agt gat gaa 365  
Glu Ser Ala Asp Ser Leu Tyr Arg Asn Ser Phe Ser Phe Ser Asp Glu  
60 65 70

aaa ctg aat tct cca aca gac tct acc cca gct ctt ctc tct gcc act 413  
Lys Leu Asn Ser Pro Thr Asp Ser Thr Pro Ala Leu Leu Ser Ala Thr  
75 80 85

gtc act cct cag aaa gct aaa tta gga gac aca aaa gag cta gaa gcc 461  
Val Thr Pro Gln Lys Ala Lys Leu Gly Asp Thr Lys Glu Leu Glu Ala  
90 95 100 105

ttc att gct gat ctt gac aaa act tta gca agt atg tgaaacaaga 507  
Phe Ile Ala Asp Leu Asp Lys Thr Leu Ala Ser Met  
110 115

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tcagctacta gaatctgctg ccagagggga caaagacgtg cactcaacct tctaccaggc 627

cactctcagg ctcaccttaa aatcagccct tgatcccatt tctgggcaat ttagacagtg 687

aaactgactt tgtttacctg cttgcagcat attagaacag acgatccatg ctaatatattgt 747

atcttctctt aaaacatagc tttcctgtaa tttaaagtgc ttttatgaaa atatttgtaa 807

ttaattatat atagttggaa atagcagtaa gctttcccat tataatatat tttgtatac 867

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&lt;211&gt; 117

&lt;212&gt; PRT

&lt;213&gt; NM\_014059 RGC32

&lt;400&gt; 78

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Ala Val Leu Ala Asp Phe Ala Ser Pro Phe His Glu Arg His Phe His  
 20 25 30

Tyr Glu Glu His Leu Glu Arg Met Lys Arg Arg Ser Ser Ala Ser Val  
 35 40 45

Ser Asp Ser Ser Gly Phe Ser Asp Ser Glu Ser Ala Asp Ser Leu Tyr  
 50 55 60

Arg Asn Ser Phe Ser Phe Ser Asp Glu Lys Leu Asn Ser Pro Thr Asp  
 65 70 75 80

Ser Thr Pro Ala Leu Leu Ser Ala Thr Val Thr Pro Gln Lys Ala Lys  
 85 90 95

Leu Gly Asp Thr Lys Glu Leu Glu Ala Phe Ile Ala Asp Leu Asp Lys  
 100 105 110

Thr Leu Ala Ser Met  
 115

&lt;210&gt; 79

&lt;211&gt; 1564

&lt;212&gt; DNA

&lt;213&gt; NM\_018004 FLJ10134

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (314)..(1138)

&lt;223&gt;

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 acccaagtgtt aaaaattcct cccccactc aatgcgagac gtggccagat cccatccaac 180  
 acacggttta attttcatgg ggctctggga tcaaaagaac agaaacagca acaacaaaag 240  
 cccagccgct gtctgatttt aagctggcaa agtgggaaaa ataaagtgtt gagtaaacag 300  
 accaagttagg atc atg ggg aat ttc aga ggt cat gcc ctc cct gga acc 349  
 Met Gly Asn Phe Arg Gly His Ala Leu Pro Gly Thr  
 1 5 10

ttc ttt ttt att att ggt ctt tgg tgg tgt aca aag agt att ctg aag Phe Phe Phe Ile Ile Gly Leu Trp Trp Cys Thr Lys Ser Ile Leu Lys 15 20 25	397
tat atc tgc aaa aag caa aag cga acc tgc tat ctt ggt tcc aaa aca Tyr Ile Cys Lys Lys Gln Lys Arg Thr Cys Tyr Leu Gly Ser Lys Thr 30 35 40	445
tta ttc tat cga ttg gaa att ttg gag gga att aca ata gtt ggc atg Leu Phe Tyr Arg Leu Glu Ile Leu Glu Gly Ile Thr Ile Val Gly Met 45 50 55 60	493
gct tta act ggc atg gct ggg gag cag ttt att cct gga ggg ccc cat Ala Leu Thr Gly Met Ala Gly Glu Gln Phe Ile Pro Gly Gly Pro His 65 70 75	541
ctg atg tta tat gac tat aaa caa ggt cac tgg aat caa ctc ctg ggc Leu Met Leu Tyr Asp Tyr Lys Gln Gly His Trp Asn Gln Leu Leu Gly 80 85 90	589
tgg cat cat ttc acc atg tat ttc ttc ttt ggg ctg ttg ggt gtg gca Trp His His Phe Thr Met Tyr Phe Phe Gly Leu Leu Gly Val Ala 95 100 105	637
gat atc tta tgt ttc acc atc agt tca ctt cct gtg tcc tta acc aag Asp Ile Leu Cys Phe Thr Ile Ser Ser Leu Pro Val Ser Leu Thr Lys 110 115 120	685
tta atg ttg tca aat gcc tta ttt gtg gag gcc ttt atc ttc tac aac Leu Met Leu Ser Asn Ala Leu Phe Val Glu Ala Phe Ile Phe Tyr Asn 125 130 135 140	733
cac act cat ggc cgg gaa atg ctg gac atc ttt gtg cac cag ctg ctg His Thr His Gly Arg Glu Met Leu Asp Ile Phe Val His Gln Leu Leu 145 150 155	781
gtt ttg gtc gtc ttt ctg aca ggc ctc gtt gcc ttc cta gag ttc ctt Val Leu Val Val Phe Leu Thr Gly Leu Val Ala Phe Leu Glu Phe Leu 160 165 170	829
gtt cgg aac aat gta ctt ctg gag cta ttg cgg tca agt ctc att ctg Val Arg Asn Asn Val Leu Leu Glu Leu Leu Arg Ser Ser Leu Ile Leu 175 180 185	877
ctt cag ggg agc tgg ttc ttt cag att gga ttt gtc ctg tat ccc ccc Leu Gln Gly Ser Trp Phe Phe Gln Ile Gly Phe Val Leu Tyr Pro Pro 190 195 200	925
agt gga ggt cct gca tgg gat ctg atg gat cat gaa aat att ttg ttt Ser Gly Gly Pro Ala Trp Asp Leu Met Asp His Glu Asn Ile Leu Phe 205 210 215 220	973
ctc acc ata tgc ttt tgt tgg cat tat gca gta acc att gtc atc gtt Leu Thr Ile Cys Phe Cys Trp His Tyr Ala Val Thr Ile Val Ile Val 225 230 235	1021
gga atg aat tat gct ttc att acc tgg ttg gtt aaa tct aga ctt aag Gly Met Asn Tyr Ala Phe Ile Thr Trp Leu Val Lys Ser Arg Leu Lys 240 245 250	1069
agg ctc tgc tcc tca gaa gtt gga ctt ctg aaa aat gct gaa cga gaa Arg Leu Cys Ser Ser Glu Val Gly Leu Leu Lys Asn Ala Glu Arg Glu 255 260 265	1117
caa gaa tca gaa gaa gaa atg tgactttgat gagcttccag tttttctaga Gln Glu Ser Glu Glu Glu Met 270 275	1168

taaacctttt cttttttaca ttgttcttgg ttttgtttct cgatcttttg tttggagaac 1228  
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 aatttaaata ttttcttttt agctttgaaa atattttggg tgatactttc attttgacac 1348  
 tcatgcacat catggtattc aggggctaga gtgatttttt tccagattat ctaaagttgg 1408  
 atgcccacac tatgaaagaa atatttgttt tatttgcctt atagatatgc tcaaggttac 1468  
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<210> 80

<211> 275

<212> PRT

<213> NM\_018004 FLJ10134

<400> 80

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 20 25 30  
 Lys Gln Lys Arg Thr Cys Tyr Leu Gly Ser Lys Thr Leu Phe Tyr Arg  
 35 40 45  
 Leu Glu Ile Leu Glu Gly Ile Thr Ile Val Gly Met Ala Leu Thr Gly  
 50 55 60  
 Met Ala Gly Glu Gln Phe Ile Pro Gly Gly Pro His Leu Met Leu Tyr  
 65 70 75 80  
 Asp Tyr Lys Gln Gly His Trp Asn Gln Leu Leu Gly Trp His His Phe  
 85 90 95  
 Thr Met Tyr Phe Phe Phe Gly Leu Leu Gly Val Ala Asp Ile Leu Cys  
 100 105 110  
 Phe Thr Ile Ser Ser Leu Pro Val Ser Leu Thr Lys Leu Met Leu Ser  
 115 120 125  
 Asn Ala Leu Phe Val Glu Ala Phe Ile Phe Tyr Asn His Thr His Gly  
 130 135 140  
 Arg Glu Met Leu Asp Ile Phe Val His Gln Leu Leu Val Leu Val Val  
 145 150 155 160



Phe Leu Thr Gly Leu Val Ala Phe Leu Glu Phe Leu Val Arg Asn Asn  
 165 170 175

Val Leu Leu Glu Leu Leu Arg Ser Ser Leu Ile Leu Leu Gln Gly Ser  
 180 185 190

Trp Phe Phe Gln Ile Gly Phe Val Leu Tyr Pro Pro Ser Gly Gly Pro  
 195 200 205

Ala Trp Asp Leu Met Asp His Glu Asn Ile Leu Phe Leu Thr Ile Cys  
 210 215 220

Phe Cys Trp His Tyr Ala Val Thr Ile Val Ile Val Gly Met Asn Tyr  
 225 230 235 240

Ala Phe Ile Thr Trp Leu Val Lys Ser Arg Leu Lys Arg Leu Cys Ser  
 245 250 255

Ser Glu Val Gly Leu Leu Lys Asn Ala Glu Arg Glu Gln Glu Ser Glu  
 260 265 270

Glu Glu Met  
 275

<210> 81

<211> 2311

<212> DNA

<213> NM\_004004 GJB2, connexin 26

<220>

<221> CDS

<222> (199)..(876)

<223>

<400> 81

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aagagttgggt gtttgctcag gaagagattt aagcatgctt gcttaccag actcagagaa 120

gtctccctgt tctgtcctag ctatgttcct gtgttggttg cattcgtctt ttccagagca 180

aaccgcccag agtagaag atg gat tgg ggc acg ctg cag acg atc ctg ggg 231  
 Met Asp Trp Gly Thr Leu Gln Thr Ile Leu Gly  
 1 5 10

ggt gtg aac aaa cac tcc acc agc att gga aag atc tgg ctc acc gtc 279  
 Gly Val Asn Lys His Ser Thr Ser Ile Gly Lys Ile Trp Leu Thr Val  
 15 20 25

ctc ttc att ttt cgc att atg atc ctc gtt gtg gct gca aag gag gtg 327

Leu Phe Ile Phe Arg Ile Met Ile Leu Val Val Ala Ala Lys Glu Val	
30 35 40	
tgg gga gat gag cag gcc gac ttt gtc tgc aac acc ctg cag cca ggc	375
Trp Gly Asp Glu Gln Ala Asp Phe Val Cys Asn Thr Leu Gln Pro Gly	
45 50 55	
tgc aag aac gtg tgc tac gat cac tac ttc ccc atc tcc cac atc cgg	423
Cys Lys Asn Val Cys Tyr Asp His Tyr Phe Pro Ile Ser His Ile Arg	
60 65 70 75	
cta tgg gcc ctg cag ctg atc ttc gtg tcc agc cca gcg ctc cta gtg	471
Leu Trp Ala Leu Gln Leu Ile Phe Val Ser Ser Pro Ala Leu Leu Val	
80 85 90	
gcc atg cac gtg gcc tac cgg aga cat gag aag aag agg aag ttc atc	519
Ala Met His Val Ala Tyr Arg Arg His Glu Lys Lys Arg Lys Phe Ile	
95 100 105	
aag ggg gag ata aag agt gaa ttt aag gac atc gag gag atc aaa acc	567
Lys Gly Glu Ile Lys Ser Glu Phe Lys Asp Ile Glu Glu Ile Lys Thr	
110 115 120	
cag aag gtc cgc atc gaa gcc tcc ctg tgg tgg acc tac aca agc agc	615
Gln Lys Val Arg Ile Glu Gly Ser Leu Trp Trp Thr Tyr Thr Ser Ser	
125 130 135	
atc ttc ttc cgg gtc atc ttc gaa gcc gcc ttc atg tac gtc ttc tat	663
Ile Phe Phe Arg Val Ile Phe Glu Ala Ala Phe Met Tyr Val Phe Tyr	
140 145 150 155	
gtc atg tac gac gcc ttc tcc atg cag cgg ctg gtg aag tgc aac gcc	711
Val Met Tyr Asp Gly Phe Ser Met Gln Arg Leu Val Lys Cys Asn Ala	
160 165 170	
tgg cct tgt ccc aac act gtg gac tgc ttt gtg tcc cgg ccc acg gag	759
Trp Pro Cys Pro Asn Thr Val Asp Cys Phe Val Ser Arg Pro Thr Glu	
175 180 185	
aag act gtc ttc aca gtg ttc atg att gca gtg tct gga att tgc atc	807
Lys Thr Val Phe Thr Val Phe Met Ile Ala Val Ser Gly Ile Cys Ile	
190 195 200	
ctg ctg aat gtc act gaa ttg tgt tat ttg cta att aga tat tgt tct	855
Leu Leu Asn Val Thr Glu Leu Cys Tyr Leu Leu Ile Arg Tyr Cys Ser	
205 210 215	
ggg aag tca aaa aag cca gtt taacgcattg cccagttggt agattaagaa	906
Gly Lys Ser Lys Lys Pro Val	
220 225	
atagacagca tgagagggat gaggcaaccc gtgctcagct gtcaaggctc agtcgccagc	966
atttcccaac acaaagattc tgaccttaaa tgcaaccatt tgaaaccctt gtaggcctca	1026
ggtgaaactc cagatgccac aatgagctct gctcccctaa agcctcaaaa caaaggccta	1086
attctatgcc tgtcttaatt ttctttcact taagttagtt ccaactgagac cccaggctgt	1146
taggggttat tgggtgaagg tactttcata ttttaaacag aggatatcgg catttgtttc	1206
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gtcctcctgg ggttcttttt gccaaacttc cccacgttaa aggtgaacat tggttctttc	1326
atttgctttg gaagttttaa tctctaacag tggacaaagt taccagtgcc ttaaactctg	1386
ttacactttt tggaagttaa aactttgtag tatgataggt tattttgatg taaagatggt	1446

ctggatacca ttatatgttc cccctgtttc agaggctcag attgtaatat gtaaattggtta 1506  
 tgtcattcgc tactatgatt taatttgaaa tatgggtcttt tggttatgaa tactttgcag 1566  
 cacagctgag agaggctgtc tgttgtatc atttggtgtca tagcacctaa caacattgta 1626  
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 tacctgtaat gacaggcctg tccaacacat ctcccttttc catgctgtgg tagccagcat 1806  
 cggaagaac gctgatttaa agagggtgagc ttgggaattt tattgacaca gtaccattta 1866  
 atggggagac aaaaatgggg gccaggggag ggagaagttt ctgtcgttaa aaacgagttt 1926  
 ggaaagactg gactctaaat tctgttgatt aaagatgagc tttgtctacc ttcaaaagtt 1986  
 tgtttggctt acccccttca gcctccaatt ttttaagtga aaatataact aataacatgt 2046  
 gaaaagaata gaagctaagg tttagataaa tattgagcag atctatagga agattgaacc 2106  
 tgaatattgc cattatgctt gacatggttt ccaaaaaatg gtactccaca tacttcagtg 2166  
 agggtaagta ttttctgtt gtcaagaata gcattgtaaa agcattttgt aataataaag 2226  
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 aacattaataa tataatctct ataatt 2311

<210> 82

<211> 226

<212> PRT

<213> NM\_004004 GJB2, connexin 26

<400> 82

Met Asp Trp Gly Thr Leu Gln Thr Ile Leu Gly Gly Val Asn Lys His  
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Ser Thr Ser Ile Gly Lys Ile Trp Leu Thr Val Leu Phe Ile Phe Arg  
 20 25 30

Ile Met Ile Leu Val Val Ala Ala Lys Glu Val Trp Gly Asp Glu Gln  
 35 40 45

Ala Asp Phe Val Cys Asn Thr Leu Gln Pro Gly Cys Lys Asn Val Cys  
 50 55 60

Tyr Asp His Tyr Phe Pro Ile Ser His Ile Arg Leu Trp Ala Leu Gln  
 65 70 75 80

Leu Ile Phe Val Ser Ser Pro Ala Leu Leu Val Ala Met His Val Ala  
 85 90 95

Tyr Arg Arg His Glu Lys Lys Arg Lys Phe Ile Lys Gly Glu Ile Lys  
 100 105 110

Ser Glu Phe Lys Asp Ile Glu Glu Ile Lys Thr Gln Lys Val Arg Ile  
 115 120 125

Glu Gly Ser Leu Trp Trp Thr Tyr Thr Ser Ser Ile Phe Phe Arg Val  
 130 135 140

Ile Phe Glu Ala Ala Phe Met Tyr Val Phe Tyr Val Met Tyr Asp Gly  
 145 150 155 160

Phe Ser Met Gln Arg Leu Val Lys Cys Asn Ala Trp Pro Cys Pro Asn  
 165 170 175

Thr Val Asp Cys Phe Val Ser Arg Pro Thr Glu Lys Thr Val Phe Thr  
 180 185 190

Val Phe Met Ile Ala Val Ser Gly Ile Cys Ile Leu Leu Asn Val Thr  
 195 200 205

Glu Leu Cys Tyr Leu Leu Ile Arg Tyr Cys Ser Gly Lys Ser Lys Lys  
 210 215 220

Pro Val  
 225

<210> 83

<211> 2389

<212> DNA

<213> NM\_002514 NOV1, neuroblastoma overexpressed gene

<220>

<221> CDS

<222> (73)..(1143)

<223>

<400> 83

gggaaggcga gcagtgccaa tctacagcga agaaagtctc gtttggtaaa agcgagaggg 60

gaaagcctga gc atg cag agt gtg cag agc acg agc ttt tgt ctc cga aag 111  
 Met Gln Ser Val Gln Ser Thr Ser Phe Cys Leu Arg Lys  
 1 5 10

cag tgc ctt tgc ctg acc ttc ctg ctt ctc cat ctc ctg gga cag gtc 159  
 Gln Cys Leu Cys Leu Thr Phe Leu Leu Leu His Leu Leu Gly Gln Val  
 15 20 25

gct gcg act cag cgc tgc cct ccc cag tgc ccg ggc cgg tgc cct gcg 207

Ala	Ala	Thr	Gln	Arg	Cys	Pro	Pro	Gln	Cys	Pro	Gly	Arg	Cys	Pro	Ala	
30					35					40					45	
acg	ccg	ccg	acc	tgc	gcc	ccc	ggg	gtg	cgc	gcg	gtg	ctg	gac	ggc	tgc	255
Thr	Pro	Pro	Thr	Cys	Ala	Pro	Gly	Val	Arg	Ala	Val	Leu	Asp	Gly	Cys	
				50					55					60		
tca	tgc	tgt	ctg	gtg	tgt	gcc	cgc	cag	cgt	ggc	gag	agc	tgc	tca	gat	303
Ser	Cys	Cys	Leu	Val	Cys	Ala	Arg	Gln	Arg	Gly	Glu	Ser	Cys	Ser	Asp	
			65					70					75			
ctg	gag	cca	tgc	gac	gag	agc	agt	ggc	ctc	tac	tgt	gat	cgc	agc	gcg	351
Leu	Glu	Pro	Cys	Asp	Glu	Ser	Ser	Gly	Leu	Tyr	Cys	Asp	Arg	Ser	Ala	
		80					85					90				
gac	ccc	agc	aac	cag	act	ggc	atc	tgc	acg	gcg	gta	gag	gga	gat	aac	399
Asp	Pro	Ser	Asn	Gln	Thr	Gly	Ile	Cys	Thr	Ala	Val	Glu	Gly	Asp	Asn	
	95					100					105					
tgt	gtg	ttc	gat	ggg	gtc	atc	tac	cgc	agt	gga	gag	aaa	ttt	cag	cca	447
Cys	Val	Phe	Asp	Gly	Val	Ile	Tyr	Arg	Ser	Gly	Glu	Lys	Phe	Gln	Pro	
110					115					120					125	
agc	tgc	aaa	ttc	cag	tgc	acc	tgc	aga	gat	ggg	cag	att	ggc	tgt	gtg	495
Ser	Cys	Lys	Phe	Gln	Cys	Thr	Cys	Arg	Asp	Gly	Gln	Ile	Gly	Cys	Val	
				130					135					140		
ccc	cgc	tgt	cag	ctg	gat	gtg	cta	ctg	cct	gag	cct	aac	tgc	cca	gct	543
Pro	Arg	Cys	Gln	Leu	Asp	Val	Leu	Pro	Glu	Pro	Asn	Cys	Pro	Ala		
			145				150					155				
cca	aga	aaa	gtt	gag	gtg	cct	gga	gag	tgc	tgt	gaa	aag	tgg	atc	tgt	591
Pro	Arg	Lys	Val	Glu	Val	Pro	Gly	Glu	Cys	Cys	Glu	Lys	Trp	Ile	Cys	
		160					165					170				
ggc	cca	gat	gag	gag	gat	tca	ctg	gga	ggc	ctt	acc	ctt	gca	gct	tac	639
Gly	Pro	Asp	Glu	Glu	Asp	Ser	Leu	Gly	Gly	Leu	Thr	Leu	Ala	Ala	Tyr	
	175					180					185					
agg	cca	gaa	gcc	acc	cta	gga	gta	gaa	gtc	tct	gac	tca	agt	gtc	aac	687
Arg	Pro	Glu	Ala	Thr	Leu	Gly	Val	Glu	Val	Ser	Asp	Ser	Ser	Val	Asn	
190					195					200					205	
tgc	att	gaa	cag	acc	aca	gag	tgg	aca	gca	tgc	tcc	aag	agc	tgt	ggc	735
Cys	Ile	Glu	Gln	Thr	Thr	Glu	Trp	Thr	Ala	Cys	Ser	Lys	Ser	Cys	Gly	
				210					215					220		
atg	ggg	ttc	tcc	acc	cgg	gtc	acc	aat	agg	aac	cgt	caa	tgt	gag	atg	783
Met	Gly	Phe		Ser	Thr	Arg	Val	Thr	Asn	Arg	Asn	Arg	Gln	Cys	Glu	Met
			225					230					235			
ctg	aaa	cag	act	cgg	ctc	tgc	atg	gtg	cgg	ccc	tgt	gaa	caa	gag	cca	831
Leu	Lys	Gln	Thr	Arg	Leu	Cys	Met	Val	Arg	Pro	Cys	Glu	Gln	Glu	Pro	
		240					245					250				
gag	cag	cca	aca	gat	aag	aaa	gga	aaa	aag	tgt	ctc	cgc	acc	aag	aag	879
Glu	Gln	Pro	Thr	Asp	Lys	Lys	Gly	Lys	Lys	Cys	Leu	Arg	Thr	Lys	Lys	
	255					260					265					
tca	ctc	aaa	gcc	atc	cac	ctg	cag	ttc	aag	aac	tgc	acc	agc	ctg	cac	927
Ser	Leu	Lys	Ala	Ile	His	Leu	Gln	Phe	Lys	Asn	Cys	Thr	Ser	Leu	His	
270					275					280					285	
acc	tac	aag	ccc	agg	ttc	tgt	ggg	gtc	tgc	agt	gat	ggc	cgc	tgc	tgc	975
Thr	Tyr	Lys	Pro	Arg	Phe	Cys	Gly	Val	Cys	Ser	Asp	Gly	Arg	Cys	Cys	
				290					295					300		
act	ccc	cac	aat	acc	aaa	acc	atc	cag	gca	gag	ttt	cag	tgc	tcc	cca	1023

Thr	Pro	His	Asn	Thr	Lys	Thr	Ile	Gln	Ala	Glu	Phe	Gln	Cys	Ser	Pro		
			305					310					315				
ggg	caa	ata	gtc	aag	aag	cca	gtg	atg	gtc	att	ggg	acc	tgc	acc	tgt		1071
Gly	Gln	Ile	Val	Lys	Lys	Pro	Val	Met	Val	Ile	Gly	Thr	Cys	Thr	Cys		
		320					325					330					
cac	acc	aac	tgt	cct	aag	aac	aat	gag	gcc	ttc	ctc	cag	gag	ctg	gag		1119
His	Thr	Asn	Cys	Pro	Lys	Asn	Asn	Glu	Ala	Phe	Leu	Gln	Glu	Leu	Glu		
		335				340					345						
ctg	aag	act	acc	aga	ggg	aaa	atg	taacctatca	ctcaagaagc	acacctacag							1173
Leu	Lys	Thr	Thr	Arg	Gly	Lys	Met										
350					355												
agcacctgta	gctgctgcgc	cacccaccat	caaaggaata	taagaaaagt	aatgaagaat												1233
cacgatttca	tccttgaatc	ctatgtat	ttt	tcctaattgtg	atcatatgag	gacctttcat											1293
atctgtcttt	tatttaacaa	aaaatgtaat	taactgtaaa	cttggaatca	aggtaagctc												1353
aggatatggc	ttaggaatga	cttactttcc	tgtgggttta	ttacaaatgc	aaatttctat												1413
aaatttaaga	aaacaagtat	ataatttact	ttgtagactg	tttcacattg	cactcatcat												1473
attttgttgt	gcactagtgc	aatccaaga	aaatatcact	gtaatgagtc	agtgaagtct												1533
agaatcatac	ttaacatttc	attgtacaag	tattacaacc	atattattgag	gttcattggg												1593
aagattctct	attggctccc	tttttgggta	aaccagctct	gaacttccaa	gctccaaatc												1653
caaggaaaca	tgcagctctt	caacatgaca	tcagagatg	actattactt	ttctgttttag												1713
ttttacacta	ggaaacgtgt	tgtatctaca	gtaatgaaat	gtttactaag	tggactgggtg												1773
tcataaaactt	tctccattta	agacacattg	actcctttcc	aatagaaaga	aactaaacag												1833
aaaactccca	atacaaaagt	gactgggtccc	tcatagccct	cagacattta	tatattggaa												1893
gctgctgagg	cccccaagtt	ttttaattaa	gcagaaacag	catattagca	gggattctct												1953
catctaactg	atgagtaaac	tgaggcccaa	agcacttgct	tacatcctct	gatagctgtt												2013
tcaaatgtgc	attttgtgga	attttgagaa	aatagagca	aatcaacat	gactgggtgt												2073
gagagaccac	acattttatg	agagtttgga	attattgtag	acatgcccaa	aacttatcct												2133
tgggccataa	ttatgaaaac	tcattgatcaa	gatatatgtg	tatacataca	tgtatctggt												2193
ttgtcagggt	acaaggtagg	ctgcaaaaatt	aaatctagac	attcttttaa	tgccaccaca												2253
cgtgttccgc	ttctctcttt	taaagtat	ttt	ataaaaatat	aaattgtaca	ttttgtaaaa											2313
tattatgttt	gatttctcta	cttgtcatat	cactaaataa	acacgatttt	attgctgaaa												2373
aaaaaaaaaa	aaaaaa																2389

&lt;210&gt; 84

&lt;211&gt; 357

&lt;212&gt; PRT

&lt;213&gt; NM\_002514 NOV1, nephroblastoma overexpressed gene

&lt;400&gt; 84

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Cys Leu Thr Phe Leu Leu Leu His Leu Leu Gly Gln Val Ala Ala Thr  
20 25 30

Gln Arg Cys Pro Pro Gln Cys Pro Gly Arg Cys Pro Ala Thr Pro Pro  
35 40 45

Thr Cys Ala Pro Gly Val Arg Ala Val Leu Asp Gly Cys Ser Cys Cys  
50 55 60

Leu Val Cys Ala Arg Gln Arg Gly Glu Ser Cys Ser Asp Leu Glu Pro  
65 70 75 80

Cys Asp Glu Ser Ser Gly Leu Tyr Cys Asp Arg Ser Ala Asp Pro Ser  
85 90 95

Asn Gln Thr Gly Ile Cys Thr Ala Val Glu Gly Asp Asn Cys Val Phe  
100 105 110

Asp Gly Val Ile Tyr Arg Ser Gly Glu Lys Phe Gln Pro Ser Cys Lys  
115 120 125

Phe Gln Cys Thr Cys Arg Asp Gly Gln Ile Gly Cys Val Pro Arg Cys  
130 135 140

Gln Leu Asp Val Leu Leu Pro Glu Pro Asn Cys Pro Ala Pro Arg Lys  
145 150 155 160

Val Glu Val Pro Gly Glu Cys Cys Glu Lys Trp Ile Cys Gly Pro Asp  
165 170 175

Glu Glu Asp Ser Leu Gly Gly Leu Thr Leu Ala Ala Tyr Arg Pro Glu  
180 185 190

Ala Thr Leu Gly Val Glu Val Ser Asp Ser Ser Val Asn Cys Ile Glu  
195 200 205

Gln Thr Thr Glu Trp Thr Ala Cys Ser Lys Ser Cys Gly Met Gly Phe  
210 215 220

Ser Thr Arg Val Thr Asn Arg Asn Arg Gln Cys Glu Met Leu Lys Gln  
225 230 235 240

Thr Arg Leu Cys Met Val Arg Pro Cys Glu Gln Glu Pro Glu Gln Pro  
245 250 255

Thr Asp Lys Lys Gly Lys Lys Cys Leu Arg Thr Lys Lys Ser Leu Lys  
260 265 270

Ala Ile His Leu Gln Phe Lys Asn Cys Thr Ser Leu His Thr Tyr Lys  
275 280 285

Pro Arg Phe Cys Gly Val Cys Ser Asp Gly Arg Cys Cys Thr Pro His  
290 295 300

Asn Thr Lys Thr Ile Gln Ala Glu Phe Gln Cys Ser Pro Gly Gln Ile  
305 310 315 320

Val Lys Lys Pro Val Met Val Ile Gly Thr Cys Thr Cys His Thr Asn  
325 330 335

Cys Pro Lys Asn Asn Glu Ala Phe Leu Gln Glu Leu Glu Leu Lys Thr  
340 345 350

Thr Arg Gly Lys Met  
355